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OM protein - protein search, using sw model.

Run on: November 15, 2000, 09:46:44 : Search time 17.97 Seconds
(without alignments)
627.933 Million cell updates/sec

Title: us-08-676-882-2

Perfect score: 1688
Sequence: 1 MAVFEKNTKPKIMVSGMT.....GSIDEVKEKQKAIADLASK 330

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A. Geneseq 36:*

- 1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseqp/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseqp/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseqp/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseqp/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseqp/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseqp/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseqp/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseqp/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseqp/AA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseqp/AA1996.DAT:*
- 18: /SIDSL/gcgdata/geneseq/geneseqp/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1685	99.8	330	18	W11476
2	828	49.1	315	15	R62605
3	828	49.1	315	20	X01690
4	706	41.8	329	17	R94013
5	421	24.9	319	12	R10591
6	412	24.4	333	9	P91948
7	403	23.9	332	10	P80891
8	398	23.6	316	20	X20054
9	397.5	23.5	314	20	X25997
10	391.5	23.2	328	12	R15736
11	391	23.1	333	18	W33107
12	390	23.1	333	18	W33108

13	371	22.0	295	20	X20055
14	356	21.1	381	20	X36058
15	352.5	20.9	298	11	R08355
16	352.5	20.9	298	11	R09295
17	271	16.1	310	12	R11119
18	240	14.2	374	20	X66184
19	238.5	14.1	338	20	X08576
20	229.5	13.6	298	20	X08577
21	204	12.1	273	18	W29773
22	157.5	9.3	148	20	X29568
23	155	9.2	327	14	R34507
24	148.5	8.8	335	20	X35684
25	143.5	8.5	339	20	X36799
26	111	6.6	36	20	X01691
27	95.5	5.7	395	16	R62956
28	95	5.6	308	21	X44811
29	92	5.5	36	20	X01692
30	91.5	5.4	470	14	R34471
31	91	5.4	470	14	R34481
32	90.5	5.4	361	18	W26001
33	89	5.3	346	20	X37730
34	87	5.2	814	16	W11940
35	86.5	5.1	361	20	X30738
36	86.5	5.1	470	14	R34479
37	86.5	5.1	470	14	R34480
38	86.5	5.1	1014	20	X34478
39	86.5	5.1	1017	20	X34477
40	86.5	5.1	1046	20	X34353
41	85	5.0	450	18	W29454
42	85	5.0	450	20	W68551
43	84	5.0	207	20	X37432
44	84	5.0	490	16	R72566
45	83.5	4.9	3163	16	R94347

ALIGNMENTS

RESULT	1
ID	W11476
W11476	standard; Protein: 330 AA.
AC	W11476:
XX	29-APR-1997 (first entry)
DE	Elmeria lactate dehydrogenase.
XX	Lactate dehydrogenase; LDH; coccidiosis; vaccine; vector.
KW	Elmeria acervulina strain Houghton.
XX	
OS	
PN	AU9656287-A.
XX	16-JAN-1997.
PD	
XX	02-JUL-1996; 96AU-0056287.
PF	
XX	03-JUL-1995; 95EP-0201801.
PR	
XX	(ALKU) AKZO NOBEL NV.
PA	
XX	kok JJ, Van Den Boogaart P, Vermeulen AN;
PI	WPI: 1997-109375/11.
DR	N-PSDB: T51370.
XX	
PT	Elmeria lactate dehydrogenase protein - used for prodn. of vaccines
XX	against coccidiosis in poultry
PS	Claim 3; Page 20-22; 30pp; English.
XX	
CC	The 37 kDa lactate dehydrogenase (LDH) (W11476) of Elmeria

CC acervulina schizonts, or immunologically active portions of it,
 CC can be used for prodn. of vaccines against coccidiosis in poultry.
 CC The LDH can be isolated from schizonts or produced in host cells or
 CC organisms transformed with recombinant vectors including LDH
 CC nucleic acids (see also T51370). Live viral vaccines can also be
 CC produced.
 CC
 XX
 SO Sequence 330 AA;

Query Match 99.8%; Score 1685; DB 18; Length 330;
 Best Local Similarity 99.7%; Pred. No. 2.5e-160;
 Matches 329; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAVENKTRPKIAMVSGMIGTMAFLCSRLRELDVLPFDVPPNMPKAMDISHNSVY 60
 DB 1 mayfektntpkiamvsgmigtmaflcsrlreldvlpfdvppnmpkamdishnsyv 60
 QY 61 DPTIITYGSSYECLEKAGADVYITTAGITKIPGSKDEKWSRMDLLPVNIKIMREYGAIRKS 120
 DB 61 dptiitygssyeclekgadvyittagitkpgskdekwsrmdllpvnikimrdygaiks 120
 QY 121 YCPNAPVINTNPLDVWVAALQESSGLPHHRICGMAGMLDSSRRPRRIADKLEVPDVO 180
 DB 121 ycpnavintnpldvwvaalqessglphhricgmagmldssrrprriadklevspdvq 180
 QY 181 GNVIGVGHDMVPLSRATVNGIPLSEFVKKGMKIOEVDIVOKTKVAGEIVRLIGOG 240
 DB 181 gnvigvghdmvplsratvngiplsefvkkgmkiOEVDIVOKTKVAGEIVRLIGOG 240
 QY 241 SATYAAGASATOMAESEYKLDKRRKRWVSCYLOGGYGVONHYLGVCVIGRGVEKITELE 300
 DB 241 sayyagasaigmaeseylkdrkrwvscylggygvonhylgvcvigrvekiitele 300
 QY 301 LTRQEROLOGSTDEYKEMOKATAALDASK 330
 DB 301 ltrqerolgstdeykenqkataaldask 330

RESULT 2

R62605 ID R62605 standard; Protein: 315 AA.

AC R62605;

DT 18-JUL-1995 (first entry)

DE P. falciparum lactate dehydrogenase.

KW Lactate dehydrogenase; LDH; immunogen; antibody; immunisation;
 KW detection; plasma; serum; malaria.

XX Plasmodium falciparum.

OS WO9424287-A.

PN WO9424287-A.

PD 27-OCT-1994.

PF 06-APR-1994; 94WO-US03796.

PR 12-APR-1993; .93US-0046160.

PA (DART-) DARTMOUTH COLLEGE.

PI Bzik DJ, Fox BA;

DR WPI, 1994-341866/42.

DR N-PSDB; Q72947.

PT Isolated gene encoding lactate dehydrogenase of P. falciparum
 PT and methods for diagnosis and vaccination against malaria

PS Claim 5; Page 18-19; 35pp; English.

XX
 CC This sequence represents P. falciparum lactate dehydrogenase (LDH).
 CC The LDH protein and immunogenic fragments of it may be used as an
 CC immunogen for antibody generation. The progress of immunisation can
 CC be monitored by detection of antibody titres in plasma or serum.
 CC Antibodies raised against fragments of LDH can be used to immunise
 CC against P. falciparum infection and to detect early malarial
 CC infection. See also R62606-14.
 CC
 XX
 SO Sequence 315 AA;

Query Match 49.1%; Score 828; DB 15; Length 315;
 Best Local Similarity 52.6%; Pred. No. 1.1e-74;
 Matches 164; Conservative 51; Mismatches 95; Indels 2; Gaps 1;

QY 9 RPKIAMVSGMIGTMAFLCSRLRELDVLPFDVPPNMPKAMDISHNSVDTGITVYG 68
 DB 4 kakivlgsgmigtmatlrvqknlgvlpfdvppnmpkaldstntvmaysnckvsg 63
 QY 69 SNSYECLEKAGADVYITTAGITKIPGSKDEKWSRMDLLPVNIKIMREYGAIRKSYCPNAPVT 128
 DB 64 snlyddlagadvvlttagitkpgskdekwrmdllpvnikimlelgthkncpafii 123
 QY 129 NITNPLDVWVAALQESSGLPHHRICGMAGMLDSSRRPRRIADKLEVPDVOGMYGVHG 188
 DB 124 vtnpvdwvaalqhsqyphknlglgvldestrlkylsqklncvprdvahivgahg 183
 QY 189 DHMVPLSRATVNGIPLSEFVKKGMKIOEVDIVOKTKVAGEIVRLIGOGSAYAPGA 248
 DB 184 dkmyllkryltvngiplsefinkklisdealelfdvtvtaletvnl--haspyvapa 241
 QY 249 SAIDMAESTYKDKRRKRWVSCYLOGGYGVONHYLGVCVIGRGVEKITELELTAOEROE 308
 DB 242 ailemaesylkdklkcstlllegqyghadifgtpvrvlgangveqleqlnseekak 301
 QY 309 LOGSIDEVKEMO 320
 DB 302 fdealeetkrmk 313

RESULT 3

Y01690 ID Y01690 standard; Protein: 315 AA.

AC Y01690;

DT 23-JUN-1999 (first entry)

DE A Plasmodium falciparum lactate dehydrogenase.

KW Lactate dehydrogenase; LDH; antibody; antigenic peptide; malaria;
 KW immunization; Plasmodium falciparum infection.

XX Plasmodium falciparum.

OS WO9913903-A1.

PN WO9913903-A1.

PD 25-MAR-1999.

PF 08-SEP-1998; 98WO-US18626.

PR 17-SEP-1997; 97US-0932194.

PA (DART-) DARTMOUTH COLLEGE.

PI Bzik DJ, Fox BA;

DR WPI, 1999-229405/19.

DR N-PSDB; X26909.

PT New antibodies to Plasmodium falciparum

PS Claim 1: Page 36-37; 46pp; English.

CC The present sequence represents a Plasmodium falciparum lactate
 CC dehydrogenase (LDH). The specification describes an antibody
 CC which binds to antigenic peptides derived from the LDH
 CC protein. The antibody can be used for diagnosing or treating
 CC malaria in a subject. The peptides and portions can be used
 CC for immunizing an individual against malaria and the antibody
 CC can also be used for diagnosing Plasmodium falciparum infections.

XX Sequence 315 AA;

Query Match 49.1%; Score 828; DB 20; Length 315;
 Best Local Similarity 52.6%; Pred. No. 1.1e-74;
 Matches 164; Conservative 51; Mismatches 95; Indels 2; Gaps 1;

OY 9 RPKIAMVSGSMIGTMAFLCSLRELDGVLEFDVVPNMPKRAMDISHNSVVDGTIVG 68
 DB 4 kaktivlgsgmlygvmatlvgknlgdvvlfdlvkmpbgkaldstlnvmaysnckvsg 63
 OY 69 SNSYECLGADVITITAGITKIPGSKDEKWSRMDLLPVNIKIREVGAIKSYCPNAFVI 128
 DB 64 sntlyddlagadvivtagftkpkqskedkewrddllplnkimletgshlkkncpnafil 123
 OY 129 NITNPLDVWVAALQESSGLPHHRICGMAGMLDSSRRRMIADKLEVSPPDVQGVNIGVHG 188
 DB 124 vltnpdvwvqllhghsgvprknlglgvidtsrlkylgysqklnvcprdnahlgahg 183
 OY 189 DHNVPLSRATVNGIPLESEFVKKWKIOEVDIYOKTKVAGEIVRLLDGSAYYAPGA 248
 DB 184 nmwvllkryltvggpldglfinmlklsdaelafdrvtvntaleynl--haaspyvapa 241
 OY 249 SAIQMAESYLKDRKRWVSCYLGQGVQVONHYLGVPCVIGRGVEKIIETELETAOER 308
 DB 242 altemaesylkdklkkvllscstllegyshtdltgtpvvlvgangvegtelqlnseek 301
 OY 309 LOGSIDEVKEMQ 320
 DB 302 fdaaiaetkrmk 313

RESULT 4
 R94013
 ID R94013 standard; Protein; 329 AA.

AC R94013;

DT 21-AUG-1996 (first entry)

DE Heat resistant maleate dehydrogenase.

KW Heat resistant maleate dehydrogenase; h-rmad; NADH; L-aspartic acid;
 alpha-ketoglutaric acid; glutamine oxalo-transaminase activity; GOT.

OS Bacillus stearothersophilus ATCC 12016.

XX Key Location/Qualifiers

FT Misc-difference 185 /note- "Given in the specification as Var"

PN JP08047389-A.

PD 20-FEB-1996.

PF 01-JUL-1994; 94JP-0151045.

PR 03-JUN-1994; 94JP-0121629.

PR 02-JUL-1993; 93JP-0164701.

PA (TOYM) TOYORO KK.

XX WPI; 1996-166248/17.

DR N-PSDB; T17715.

PT Protein having heat resistant maleate dehydrogenase activity - and
 PT reagent cong. protein, NADH and L-aspartic and alpha-keto-glutaric
 PT acid for determination of glutamine oxalo-transaminase activity

PS Claim 8; Page 13-15; 17pp; Japanese.

CC This sequence represents a protein having heat resistant maleate
 CC dehydrogenase (h-rmad) activity. The protein has a residual activity
 CC after storage at 40 deg.C for 10 days of at least 60%, pref. 70%
 CC and esp. 90%. A reagent containing the h-rmad protein, NADH and L-
 CC aspartic and alpha-ketoglutaric acid may be used for the
 CC determination of glutamine oxalo-transaminase (GOT) activity. The h-
 CC rmad protein may be produced by transforming E. coli with the DNA
 CC encoding this protein and isolating the protein from the culture medium.

XX Sequence 329 AA;

Query Match 41.8%; Score 706; DB 17; Length 329;
 Best Local Similarity 45.3%; Pred. No. 1.9e-62;
 Matches 136; Conservative 64; Mismatches 88; Indels 12; Gaps 3;

OY 9 RPKIAMVSGSMIGTMAFLCSLRELDGVLEFDV--VPNMPKRAMDISHNSVVDGTIV 66
 DB 5 rktsivlgagftgatafliaqkelgdvvlvdipqlenptkylalmleaspyvlgfani 64
 OY 67 YGSNYSYECGADVITITAGITKIPGSKDEKWSRMDLLPVNIKIREVGAIKSYCPNAF 126
 DB 65 lgtadyadladsdivltagarkpg-----msrdjltvntqklnkgytkevkvyspncy 119
 OY 127 VINTNPLDVWVAALQESSGLPHHRICGMAGMLDSSRRRMIADKLEVSPPDVQGVNIGV 186
 DB 120 lvtvnpdvdamlylvfkesgfpknrvlgsgvidtarftfveeehlsvdkvlgfvlg 179
 OY 187 HGDHNPVLSRATVNGIPLESEFVKKWKIOEVDIYOKTKVAGEIVRLLDGSAYYAP 246
 DB 180 hgddmvpvlvrysyagplpleklpk-----dridaivertckgggelyvnlngnsayap 234
 OY 247 GASAIQMAESYLKDRKRWVSCYLGQGVQVONHYLGVPCVIGRGVEKIIETELETAOER 306
 DB 235 aasivemveallkdkrrllpalaylegeygyglvlyprrllgngltxkyleleeteek 294

RESULT 5

R10591
 ID R10591 standard; Protein; 319 AA.

AC R10591;

DT 20-MAR-1991 (first entry)

DE L-lactic acid dehydrogenase.

KW LDH; L-lactic acid; thermophile.

OS Bacillus strain TP-262.

PN JP02286077-A.

PD 26-NOV-1990.

PF 27-APR-1989; 89JP-0108432.

PR 27-APR-1989; 89JP-0108432.

PA (TOYA) TOYAMA CHEM KK.

XX WPI; 1991-012213/02.

DR O-PSDB; Q10162.

XX Bacillus sp. pref. TP-262 strain - is thermophilic bacterium

PT producing L-lactic acid dehydrogenase.

XX Disclosure: Fig 1, 16pp; Japanese.

CC The sequence was deduced from DNA which can be used to produce
CC L-LDH by recombinant DNA techniques. The bacillus species contg.
CC the DNA and able to express it is new and is thermophilic, growing
CC at 50-70 deg.C.

XX Sequence 319 AA:

Query Match 24.9%; Score 421; DB 12; Length 319;
Best Local Similarity 27.9%; Pred. No. 5,6e-34;
Matches 87; Conservative 88; Mismatches 125; Indels 12; Gaps 7;

QY 11 KIAMVSGMIGTMAFLCRLRELD-VLFDVVPNMPKMGKADISHNSVVDGTVGSG 69
DB 8 rva11gtetvgasyafalmngjadelv1dvkkaegdvmdlnhgkfvapkm1wng 67
QY 70 NSEELKAGDVVITTAGITKIRGSKSDKMSRMDLLFVNKIMRE-VGAAIKSYCPNAPVI 128
DB 68 dygdc-qdadlvvicagangkpge-----trldvknmmikfk1vdsvmksqfddg1flv.121
QY 129 NITNPLDVVVAALQESSGLPHIRICGMAGMLDSSRFRMIADKLESPRDVOCMTVGHG 188
DB 122 -atnpvdil1yctwkfsg1pkcv1gsgcltdatrf1vsefyfqpvpnvahay1lgehg 180
QY 189 DHMVLRSRYATVNGIPLESEFKKG-WIKOEVDVDTQKTKVAGETVRLGOGSAVYAG 247
DB 181 dte1pwtshaelsgvplieg1lsqndryrkedlen1fvnrdaaayvie--kgaetyyga 238
QY 248 ASATMAESYLDKRRKRWVCSCYLOGQGVONHVLGVPVCVIGRGVEKIIIELELTAOERO 307
DB 239 mglv1itral1hmenal1tvsayldg1yqnegvny1vpa1lnrng1fremelk1lne1eq 298
QY 308 ELQGSIDEVKEK 319
DB 299 qthhsvtv1kdl 310

RESULT 6
P91948 ID P91948 standard; protein: 333 AA.

XX AC P91948;
XX DT 16-FEB-1990 (first entry)
XX DE Pig H4 isoenzyme.
XX KW NAD-dependent lactate dehydrogenase; H4 isoenzyme.
XX OS Suidae.
XX FH Key Location/Qualifiers
FT Binding-site 98..110
FT Binding-site /note="substrate recognition site."
FT Binding-site 167..173
FT Misc-difference 102..102 /note="activator site."
FT Misc-difference 102..102 /note="basic AA."
FT Misc-difference 173..173 /note="basic AA."
XX MO8908707-A.

XX PD 21-SEP-1989.
XX PF 16-MAR-1989; 89WD-GB00279.
XX PR 17-MAR-1988; 88GB-0006358.

PA (UYBR-) UNIVERSITY OF BRISTOL.

XX Holbrook JJ, Clarke AR, Atkinson A;

XX WPL; 1989-292522/40.

PT Recombinant NAD-dependent dehydrogenase - which interconverts malate
PT and oxaloacetate, and has low dependence on fructose-1,6-biphosphate
PT as activator.

PS Disclosure: page 4-5; 25pp; English.

CC Sequence codes for the H4 isoenzyme of pig - an NAD-dependent lactate
CC dehydrogenase. It is used to construct a recombinant enzyme in which
CC AAl02 and AAl73 are basic, esp. Arg, and Gln resp. The mutation of AAl02
CC results in the creation of a malate dehydrogenase from the lactate
CC dehydrogenase framework, the mutation being on the mobile coenzyme loop
CC and changing the substrate binding specificity of the protein. The
CC mutation of AAl73, which is in the activation site, decreases
CC sensitivity of the protein to activation by sugar phosphates.

XX Sequence 333 AA:

Query Match 24.4%; Score 412; DB 10; Length 333;
Best Local Similarity 29.9%; Pred. No. 4,7e-33;
Matches 101; Conservative 73; Mismatches 130; Indels 34; Gaps 10;

QY 5 EKTTRP-KIAMVSGMIGTMAFLCRLRELG-----DVVLFDPVNPMPKMGKADISHNS 57
DB 14 get1lphnk1lvvgvgv-----macalsilgsltdelalvd1edk1kgemmd1qhs 69
QY 58 SVYDGTGVGSGSYCLMGADVITTAGITKIRGSKSDKMSRMDLLFVNKIMREYGAA 117
DB 70 lf1qcp-k1vanmdyvtanskivlvv1agv1qgege-----st1nlvqrvnv1fkf1lpq 123
QY 118 IRKSYCPNAPVINTNPLDVVVAALQESSGLPHIRICGMAGMLDSSRFRMIADKLESPR 177
DB 124 lvy1spnc1l1v1spvd1l1yctwk1sg1pkhrv1gsgcn1dsatf1ymaek1gvhs 183
QY 178 DVQGVN1GVGHDMVPLSRVATVNGIPLESEF-----VKKQIMOEVDVDTQKTKVA 229
DB 184 sc1hgy1l1g1ghd1sv1v1g1v1g1q1npemg1td1nd1senw---kevh1mvesay- 239
QY 230 GGEIVL1LGOGSAVYAPGASATMAESYLDKRRKRWVCSCYLOGQGVONH-YLGVPVY 288
DB 240 --ev1kl--k1y1twa1g1svad1lesm1k1n1str1pvt1m1vgm1y1enev1f1spcv1 295
QY 289 GGRGVEKIIIELELTAOEROELQGSIDEVKEKMAIAL 326
DB 296 narg1t1sv1ngk1k1d1evag1k1nsad1t1wg1qk1d1kdl 333

RESULT 7
P80891 ID P80891 standard; protein: 332 AA.

XX AC P80891;

XX DT 29-NOV-1990 (first entry)

XX DE Testis-specific lactate dehydrogenase subunit LDH-C4.

XX KW Testis-specific lactate dehydrogenase; vaccine; female fertility.

XX OS synthetic.

XX EP270056-A.

XX PD 08-JUN-1988.

XX PF 30-NOV-1987; 87EP-0117688.

Query Match	23.9%	Score 403	DB 9	Length 332
Best Local Similarity	30.9%	Pred. No.	3.7e-32	
Matches 101	Conservative 72	Mismatches 130	Indels 24	Gaps 7

RESULT	8
Y20054	
ID	Y20054 standard; Protein; 316 AA.
XX	
AC	Y20054;
XX	
DT	19-JUL-1999 (first entry)
DE	B. burgdorferi antigenic protein, f874.aa.
KM	Antigenic protein; vaccine; Lyme disease; infection; detection.
XX	
OS	Borrelia burgdorferi.
PN	WO9859071-A1.
XX	
PD	30-DEC-1998.
XX	
PF	18-JUN-1998; 98WO-US12718.
XX	

Query Match	23.68;	Score 398;	DB 20;	Length 316;
Best Local Similarity	27.48;	Pred. No. 1.1e-31;		
Matches 87;	Conservative 89;	Mismatches 117;	Indels 24;	Gaps 8

RESULT	9
Y25997	
ID	Y25997 standard; Protein; 314 AA.
XX	
AC	Y25997;
XX	
DT	18-OCT-1999 (first entry)
XX	
DE	B. flavum lactate dehydrogenase protein.
XX	
KM	Lactate dehydrogenase: destruction; lactic acid.
XX	
OS	Brevibacterium flavum.
XX	

PN JP11206385-A.
XX
PD 03-AUG-1999.
XX
PF 28-JAN-1998; 98JP-0030594.
XX
PR 28-JAN-1998; 98JP-0030594.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
DR WPI; 1999-486360/41.
DR N-PSDB; Z09139.
XX
PT New lactate dehydrogenase gene and strain destroying gene - useful
PT for formation of lactic acid
PS
PS Claim 1; Page 11-12; 13pp; Japanese.
XX
XX This invention describes the isolation of a novel lactate dehydrogenase
CC protein from Brevibacterium flavum strain Mj-233. The invention also
CC describes a microbial strain destroying the lactate dehydrogenase gene of
CC a microbe in which the lactate dehydrogenase gene is destroyed by a
CC homologous recombination of the above DNA or the above recombinant vector
CC DNA with the lactate dehydrogenase gene on the chromosome DNA of the
CC microbe cell and a method for the preparation of an amino acid or an
CC organic acid in which the above strain destroying the lactate
CC dehydrogenase gene is cultured in a medium and the amino acid or the
CC organic acid (except lactic acid) is collected from the culture.
CC Formation of lactic acid in the preparation of an amino acid and an
CC organic acid can be decreased with no control of oxygen concentration
CC during culture. This sequence represents the lactate dehydrogenase
CC protein described in the specification.
XX
SQ Sequence 314 AA:

Query Match 23.5%; Score 397.5; DB 20; Length 314;
Best Local Similarity 29.7%; Pred. No. 1.2e-31;
Matches 93; Conservative 76; Mismatches 133; Indels 11; Gaps 6;
QY 11 KIAMVSGMIGTMAFLCSTRELGD-VLFEDVVPNMPKRAMDISHNSVVDGTGYGS 69
DB 8 KAVLIGAGVGVAYAYALLNGMADHAIIDIDDKLEGVMDLNBGVVADSTRVTKG 67
QY 70 NSEELCKAGDVVITTAGITIKIPKSDKEMRMDLPPVNIKIMRE-VGAIKSYCPNAEVI 128
DB 68 LYADC-EDAMVVICAGAAQKPGE-----LRLQIVKKNVIMKISIVGVNASGFDGIFLV 121
QY 129 NITNPLDVVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPPVQGMVIGVHG 188
DB 122 -ASNPDLITLVAVKTSGLIEMNIVISGLVDSARITVMIGELYEVAAPSVHAYILIGEHG 180
QY 189 DHMVPISRYATVNGIPLSEFVKKGMIKOEVEDIVOKTKVAGEIYVLLQGSAYVAFPA 248
DB 181 dteLpLsatslaagvslsmldkpeLgrlekIfedtrdaayhld--akgstsyiglm 238
QY 249 SAIDMAESTLYKDRKRWVSCYLOGOYGVONHLYGVCVIGGKVEKIIELELTADQROE 308
DB 239 gJarltRatqIqndvaavpvsallhgeyedIyIgpavvnrgItrVveltdhemer 298
QY 309 LOGSIDEVEMOK 321
DB 299 fKhsantlreiqk 311

RESULT 10
ID R15736 standard; Protein: 328 AA.
XX R15736;
AC R15736;
DE 17-MAR-1992 (first entry)
DT
XX

DE L-lactic acid dehydrogenase.
XX
XX Recombinant.
KM
XX
XX Streptococcus thermophilus.
OS
XX
XX JP03251172-A.
PN
XX
XX 08-NOV-1991.
PD
XX
XX 28-FEB-1990; 90JP-0045967.
PF
XX
XX 28-FEB-1990; 90JP-0045967.
PR
XX
XX (MEIP) MEIJI MILK PRODS KK.
PA
XX
XX WPI; 1991-373410/51.
DR N-PSDB; Q15280.
XX
XX
XX New L-lactic acid dehydrogenase and gene encoding it - for
PT producing L-lactic acid in vitro in high yield from pyruvic acid
PT
XX
XX Claim 1; Fig 1; 9pp; Japanese.
PS
XX
XX The sequence is that of a new L-lactic acid dehydrogenase which may
CC produced in large amts. The enzyme can produce lactic acid in vitro
CC from pyruvic acid and may be produced directly by culturing a
CC transformed bacteria in which the gene is introduced.
XX
SQ Sequence 328 AA:

Query Match 23.2%; Score 391.5; DB 12; Length 328;
Best Local Similarity 29.2%; Pred. No. 5.2e-31;
Matches 92; Conservative 75; Mismatches 127; Indels 21; Gaps 7;
QY 11 KIAMVSGMIGTMAFLC-----SRELGDVLFEDVVPNM--PMKRAMDISHNSVVDTG 63
DB 9 KAVLIGAGVGVAYAYALLNGMADHAIIDIDDKLEGVMDLNBGVVADSTRVTKG 62
QY 64 ITVGSNSYELCKAGADVITTAGITIKIPKSDKEMRMDLPPVNIKIMREYGAIAIKSYCP 123
DB 63 PKIYAACKYACDADLVLTGAPGKPGE-----LRLDIVGKRLANKSIVGVESGF 117
QY 124 NAEVINITNPLDVVAALQESSGLPHHRICGMAGMLDSSRRFRMIADKLEVSPPVQGMV 183
DB 118 ngflvvaanpvdvltystwtfsgftrkervlvgstslsatsrtqalaeKlnvdarsvnyi 177
QY 184 IGVHGDHMPVLSRYATVNGIPLSEFVK-KGMIKOEVEDIVOKTKVAGEIYVLLQGS 242
DB 178 mgehgdsfawshaniagvnlleflkdenvgaeelvelfegvridaaytlm--kkgat 235
QY 243 YVAPGASAIOMAESYLKDRKRWVSCYLOGOYGVONHLYGVCVIGGKVEKIIELELT 302
DB 236 YyglavalaratKallddenavipLsvfgegyqyvmnlffigpaIyabhlvrvpnpln 295
QY 303 AOEFOELGOSIDEVK 317
DB 296 daeqqmkasadelq 310

RESULT 11
ID W33107 standard; Protein: 333 AA.
XX W33107;
AC W33107;
DE 28-JAN-1998 (first entry)
DT
XX
XX Chicken lactic acid dehydrogenase type B subunit.
XX
XX Chicken lactic acid dehydrogenase; LDH; type B subunit; tetramer;
KM CUDH-B4 isozyme; reagent; transaminase; determination.

XX Gallus domesticus.
 OS JP09262089-A.
 XX
 XX 07-OCT-1997.
 PD
 XX 28-MAR-1996; 96JP-0073797.
 PF
 XX 28-MAR-1996; 96JP-0073797..
 PR
 XX (ORIV) ORIENTAL YEAST CO LTD.
 XX
 XX WPI: 1997-544152/50.
 DR N-PSDB; T88365.
 XX
 XX DNA encoding chicken lactic acid dehydrogenase type B subunit -
 PT which can form tetramer, useful as reagent for transaminase activity
 PT determination
 XX
 XX Claim 1; Pages 9-10; 16pp; Japanese.
 PS
 XX The present sequence is chicken lactic acid dehydrogenase
 CC (LDH) type B subunit, which can form a tetramer to give CLDH-B4
 CC isozyme. The CLDH-B4 isozyme can be used as a reagent for
 CC transaminase activity determination.
 CC
 SQ Sequence 333 AA;

Query Match 23.28; Score 391; DB 18; Length 333;
 Best Local Similarity 29.98; Pred. No. 6e-31;
 Matches 97; Conservative 69; Mismatches 138; Indels 20; Gaps 8;

OY 11 KIAWGSIGMGICMAFLCSLRELG----DVLFEDVPPNMPGKAMDISHNSVVDGIGT 65
 DB 22 KILVGVGVGVG---macalsilgkglcdelaivdvledkikgemmdlqhsiflqth-k 76
 OY 66 VYGSNSYECLKGAADVITTAGITKIPGKSDKESRMDLFPVNIKIMREVGAAIKSYCPNA 125
 DB 77 Ivaadkyavtanskilvvvtagvtrqgege-----srlnlvqnnvvefkilpqivkyspnc 131
 OY 126 FVINTNPDLVMAALQESSGLPHNRICGMAGMDSSRFRRMADKLEVSPPDVQGVYIG 185
 DB 132 ILLVSNPVDLLIYVTKLSGLPRKRVIGSGNDLtarfrylmaerlgihtschgwilg 191
 OY 186 VHGDHMPPLSRATVNGIPSEF-VKKGWIKQEVDDIVQKTVAGG-ETVRLLGQGSAY 243
 DB 192 ehgdsavavsgvnnvavslqdelnpamgtcdksenwkevhkqvvesayevirl--kgytn 249
 OY 244 YAPGASAIOMAESYLKDRKRVWCSCYLOGGYGVONH-YGVPCVIGRGVEKILELELT 302
 DB 250 waiglsvaelcelmknlyrvhsvtlvkgytgiendvflispcvlasaagltsvinqklk 309
 OY 303 AQERQELQGSIDEVKEKOKAIAAL 326
 DB 310 ddevaqlkksadtlwsiqdkldl 333

RESULT 12
 ID W33108 standard; Protein: 333 AA.
 XX
 AC W33108;
 XX
 XX 28-JAN-1998 (first entry)
 DT
 XX Chicken lactic acid dehydrogenase type B subunit.
 DE
 XX Chicken lactic acid dehydrogenase; LDH; type B subunit; tetramer;
 XX CLDH-B4 isozyme; reagent; transaminase; determination.
 KM
 XX Gallus domesticus.
 OS

XX JP09262089-A.
 XX
 XX 07-OCT-1997.
 PD
 XX 28-MAR-1996; 96JP-0073797.
 PF
 XX 28-MAR-1996; 96JP-0073797..
 PR
 XX (ORIV) ORIENTAL YEAST CO LTD.
 XX
 XX WPI: 1997-544152/50.
 DR
 XX DNA encoding chicken lactic acid dehydrogenase type B subunit -
 PT which can form tetramer, useful as reagent for transaminase activity
 PT determination
 XX
 XX Claim 1; Pages 10-11; 16pp; Japanese.
 PS
 XX The present sequence is chicken lactic acid dehydrogenase
 CC (LDH) type B subunit, which can form a tetramer to give CLDH-B4
 CC isozyme. The CLDH-B4 isozyme can be used as a reagent for
 CC transaminase activity determination.
 CC
 SQ Sequence 333 AA;

Query Match 23.18; Score 390; DB 18; Length 333;
 Best Local Similarity 29.68; Pred. No. 7.5e-31;
 Matches 96; Conservative 70; Mismatches 138; Indels 20; Gaps 8;

OY 11 KIAWGSIGMGICMAFLCSLRELG----DVLFEDVPPNMPGKAMDISHNSVVDGIGT 65
 DB 22 KILVGVGVGVG---macalsilgkglcdelaivdvledkikgemmdlqhsiflqth-k 76
 OY 66 VYGSNSYECLKGAADVITTAGITKIPGKSDKESRMDLFPVNIKIMREVGAAIKSYCPNA 125
 DB 77 Ivaadkyavtanskilvvvtagvtrqgege-----srlnlvqnnvvefkilpqivkyspnc 131
 OY 126 FVINTNPDLVMAALQESSGLPHNRICGMAGMDSSRFRRMADKLEVSPPDVQGVYIG 185
 DB 132 ILLVSNPVDLLIYVTKLSGLPRKRVIGSGNDLtarfrylmaerlgihtschgwilg 191
 OY 186 VHGDHMPPLSRATVNGIPSEF-VKKGWIKQEVDDIVQKTVAGG-ETVRLLGQGSAY 243
 DB 192 ehgdsavavsgvnnvavslqdelnpamgtcdksenwkevhkqvvesayevirl--kgytn 249
 OY 244 YAPGASAIOMAESYLKDRKRVWCSCYLOGGYGVONH-YGVPCVIGRGVEKILELELT 302
 DB 250 waiglsvaelcelmknlyrvhsvtlvkgytgiendvflispcvlasaagltsvinqklk 309
 OY 303 AQERQELQGSIDEVKEKOKAIAAL 326
 DB 310 ddevaqlkksadtlwsiqdkldl 333

RESULT 13
 ID Y20055 standard; Protein: 295 AA.
 XX
 AC Y20055;
 XX
 XX 19-JUL-1999 (first entry)
 DT
 XX B. burgdorferi antigenic protein, t874.aa.
 DE
 XX Antigenic protein; vaccine; Lyme disease; infection; detection.
 XX Borrelia burgdorferi.
 OS
 XX WO9859071-A1.
 XX
 PD 30-DEC-1998.

Search completed: November 15, 2000, 09:48:27
Job time: 103 sec

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Query Match      20.9%   Score 352.5; DB 11; Length 296;
Best Local Similarity 25.6%   Pred. No. 3, 6e-27;
Matches    81; Conservative    70; Mismatches 138; Indels    27; Gaps    5

OY      5 EKNTPRKFAAMGSGMIGCTMAFLCLSLRELD-VLEFDVVPNNMKCAMDISHNSVVDTG 63
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2 knngatgrrvvlgagfvgasgyfalnmqgladelvilldaneskaigdamfnbgkfaprk 61
OY     64 ITVGGSNVEYCCKAGADVVTITAGTTRPKPSKDEMSRMLLPNNIKIMEVGAALISYCP 123
       ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     62 vdiwmgdyddc-rdddlvlvicagankpkpe-----rlidvdkkalfstgsxrllmasgf 115
OY    124 NAEVINTPRLDVWVALAEOESSGLRPNRIICGNAGMWIDSSRFPMRIDKTEVSPRDQGW 183
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    116 qallfvacnprdlllyuatcklsglrpherylsgrllldtarfflllgeylsvldatarfayl 175
OY    184 IGVHGDHNMPVRATVATNGIRPLSEFVKKKGMIOEEDVDIVQRTKVAGGETVLRLGGGSAY 243
       ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    176 lgehnddtelrv-----wsaqakdelrfvnvdadayaqlle--kkyga 215

```

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OM protein - protein search, using sw model

Run on: November 15, 2000, 09:46:44 ; Search time 26.25 Seconds
(without alignments)
210.712 Million cell updates/sec

Title: US-08-676-882-2

Perfect score: 1688
Sequence: 1 MAVFEKTRPKIAMVSGMT.....GSTDEVKEMOKAIALDASK 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCITUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	100.0	330	3	US-08-676-882-2
2	828	49.1	315	4	PCT-US94-03796-2
3	706	41.8	329	1	US-08-270-013B-2
4	706	41.8	329	1	US-08-838-418-2
5	412	24.4	317	1	US-08-748-068-3
6	412	24.4	333	1	US-08-748-068-1
7	391	23.2	333	2	US-08-869-506-2
8	391	23.2	333	3	US-08-128-967-2
9	390	23.1	333	2	US-08-869-506-3
10	390	23.1	333	3	US-09-128-967-3
11	377.5	22.4	327	1	US-07-748-068-2
12	155	9.2	327	1	US-08-211-682-25
13	87	5.2	814	1	US-08-286-305A-3
14	87	5.2	814	2	US-08-441-104A-3
15	87	5.2	814	3	US-08-440-816A-3
16	85	5.0	450	1	US-08-665-435A-2
17	85	5.0	450	2	US-08-843-309-2
18	84.5	5.0	549	3	US-08-886-886-13
19	84.5	5.0	3491	2	US-07-642-734C-2
20	84.5	5.0	3491	3	US-08-439-009A-2
21	84	5.0	351	3	US-08-886-886-15
22	83	4.9	20	4	PCT-US94-03796-8
23	82.5	4.9	391	1	US-08-759-581B-13
24	82.5	4.9	934	1	US-08-215-805A-80
25	81.5	4.8	396	3	US-08-926-253-2
26	81.5	4.8	396	3	US-09-120-074-2
27	81.5	4.8	438	3	US-08-886-886-2
28	81.5	4.8	883	1	US-08-106-433A-2

29	81	4.8	446	2	US-08-934-481-2	Sequence 2, Appli
30	80	4.7	396	2	US-09-061-337-12	Sequence 12, Appl
31	80	4.7	396	2	US-09-122-129-12	Sequence 12, Appl
32	80	4.7	396	3	US-09-340-991-12	Sequence 12, Appl
33	80	4.7	511	3	US-08-931-952-4	Sequence 4, Appli
34	80	4.7	511	3	US-08-272-247-4	Sequence 4, Appli
35	80	4.7	511	4	PCT-US95-08560-4	Sequence 4, Appli
36	79	4.7	418	3	US-08-844-054-2	Sequence 2, Appli
37	79	4.7	453	1	US-08-374-155A-8	Sequence 8, Appli
38	79	4.7	453	1	US-08-785-396-8	Sequence 8, Appli
39	79	4.7	3033	1	US-07-923-693-5	Sequence 5, Appli
40	78.5	4.7	396	1	US-07-702-771-1	Sequence 1, Appli
41	78.5	4.7	443	2	US-08-935-450-6	Sequence 6, Appli
42	78.5	4.7	1313	3	US-08-244-537-2	Sequence 2, Appli
43	78	4.6	422	4	PCT-US91-01360-2	Sequence 2, Appli
44	78	4.6	746	2	US-08-785-431-4	Sequence 2, Appli
45	78	4.6	788	2	US-08-785-431-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-08-676-882-2
; Sequence 2, Application US/08676882
; Patent No. 6100241
; GENERAL INFORMATION:
; APPLICANT: Kok, Jacobus Johannes
; APPLICANT: van den Boogaart, Paul
; APPLICANT: Vermeulen, Arnoldus Nicolaas
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Akzo No. 6100241el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/676, 882
; APPLICATION NUMBER: US/08/676, 882
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gornley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; TELEFAX: (301) 977-0847
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-676-882-2

Query Match 100.0%; Score 1688; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.2e-177;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAVFEKTRPKIAMVSGMTAFLCSLRELGVVLEDDVVPNNPMKRAMDISNSSVY 60
DB 1 MAVFEKTRPKIAMVSGMTAFLCSLRELGVVLEDDVVPNNPMKRAMDISNSSVY 60
OY 61 DTGIVVGSNSECKGADVITITGIRKCKSKKMSRMDLFPVNIKIREVCAAKS 120
|||||
```

Db 61 DTGTVGSGNSYECLKGADVITITAGITKIPGKSDKEMSRMDLLPVNIKIMREVGAAIKS 120
OY 121 YCPNFAVINTNPDLVMAALQESSGLPHHRICGAGMLDSSFRFMIADKLEVSFRDVO 180
Db 121 YCPNFAVINTNPDLVMAALQESSGLPHHRICGAGMLDSSFRFMIADKLEVSFRDVO 180
OY 181 GNVICVGHDMVPLSRATVNGICPLSEFVKKGMKIOEVDVDTVOKTKVAGGELVRLGSG 240
Db 181 GNVICVGHDMVPLSRATVNGICPLSEFVKKGMKIOEVDVDTVOKTKVAGGELVRLGSG 240
OY 241 SAYAPGASAIQMAESYIKDKRRKRVWVSCYLOGGVONHVLGVPCVIGRGVEKIEELE 300
Db 241 SAYAPGASAIQMAESYIKDKRRKRVWVSCYLOGGVONHVLGVPCVIGRGVEKIEELE 300
OY 301 LTAEROELQSGIDBVKEMOKAIAALDASK 330
Db 301 LTAEROELQSGIDBVKEMOKAIAALDASK 330
RESULT 2
PCT-US94-03796-2
Sequence 2, Application PC/TUS9403796
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: GENE ENCODING THE LACTATE DEHYDROGENASE
TITLE OF INVENTION: ENZYME OF PLASMIDIUM FALCIPARUM
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03796
FILING DATE: 06-APR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/046,160
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: DCI-066CPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-03796-2

Query Match 49.1%; Score 828; DB 4; Length 315;
Best Local Similarity 52.6%; Pred. No. 5,9e-83;
Matches 164; Conservative 51; Mismatches 95; Indels 2; Gaps 1;

OY 9 RPKIAMVSGMIGTMAFLCSLRELGDVYLFVDPVPMKRAMDISNSSVVDGITYVG 68
Db 4 KAKIVLVGSMIGVATLLVOKNLGDVYLFVDPVPMKRAMDISNSSVVDGITYVG 68
OY 69 SNSEYELKAGADVITITAGITKIPGKSDKEMSRMDLLPVNIKIMREVGAAIKSYCPNFAVI 128
Db 64 SNSEYELKAGADVITITAGITKIPGKSDKEMSRMDLLPVNIKIMREVGAAIKSYCPNFAVI 128
OY 129 NITNPDLVMAALQESSGLPHHRICGAGMLDSSFRFMIADKLEVSFRDVOGVNIGV 188
Db 124 VTNPDVMAALQESSGLPHHRICGAGMLDSSFRFMIADKLEVSFRDVOGVNIGV 188
OY 189 DHNVPLSRATVNGICPLSEFVKKGMKIOEVDVDTVOKTKVAGGELVRLGSGSAYAPGA 248
Db 189 DHNVPLSRATVNGICPLSEFVKKGMKIOEVDVDTVOKTKVAGGELVRLGSGSAYAPGA 248

Db 184 NKKVLLKRTYVGGIPLQEFINNKLSDALEAIFDRVTATALEIVNL--HASPYVAPPA 241
OY 249 SAIQMAESYIKDKRRKRVWVSCYLOGGVONHVLGVPCVIGRGVEKIEELELTAEROEL 308
Db 242 AITEMAESTLKDKKVLICSTLLEGGHSDIFGTPVVLGANGVQVIELQINSEKAK 301
OY 309 LOGSIDBVKEMOK 320
Db 302 FDEAIAETKRMK 313

RESULT 3
US-08-270-013B-2
Sequence 2, Application US/08270013B
Patent No. 5686294
GENERAL INFORMATION:
APPLICANT: Sogabe et al.
TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 61601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,013B
FILING DATE: 01-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 164701/1993
FILING DATE: 02-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Green, Robert F.
REGISTRATION NUMBER: 27555
REFERENCE/DOCKET NUMBER: 62321
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: (425)3533
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-270-013B-2

Query Match 41.8%; Score 706; DB 1; Length 329;
Best Local Similarity 45.3%; Pred. No. 1,7e-69;
Matches 136; Conservative 64; Mismatches 88; Indels 12; Gaps 3;

OY 9 RPKIAMVSGMIGTMAFLCSLRELGDVYLFVDPVPMKRAMDISNSSVVDGITYVG 66
Db 5 RPKIAMVSGMIGTMAFLCSLRELGDVYLFVDPVPMKRAMDISNSSVVDGITYVG 66
OY 67 YGNSYELKAGADVITITAGITKIPGKSDKEMSRMDLLPVNIKIMREVGAAIKSYCPNFAVI 126
Db 65 YGNSYELKAGADVITITAGITKIPGKSDKEMSRMDLLPVNIKIMREVGAAIKSYCPNFAVI 126
OY 127 VITNPDLVMAALQESSGLPHHRICGAGMLDSSFRFMIADKLEVSFRDVOGVNIGV 186
Db 120 VITNPDLVMAALQESSGLPHHRICGAGMLDSSFRFMIADKLEVSFRDVOGVNIGV 186
OY 187 HGDHNVPLSRATVNGICPLSEFVKKGMKIOEVDVDTVOKTKVAGGELVRLGSGSAYAP 246
Db 187 HGDHNVPLSRATVNGICPLSEFVKKGMKIOEVDVDTVOKTKVAGGELVRLGSGSAYAP 246

Db 180 HGDMVPLVRSYAGIPILEKTIIPK-----DRDAIVERTKGGGEIYNLNGNSAYIAP 234
OY 247 GASAIOMAESEILKRRKRVMSCTILOGOYQVONHYLGPVCIYGRGVKRIIELELTAOR 306
Db 235 AASLIVENEAELIKDORILPAIAYLEGEYEGYIGVPTILGNGIEKVEIELELTEEK 294

RESULT 4

US-08-838-418-2
Sequence 2, Application US/08838418
Patent No. 5744342
GENERAL INFORMATION:
APPLICANT: Sogabe et al.
TITLE OF INVENTION: PROTEIN HAVING HEAT-RESISTANT MALATE
TITLE OF INVENTION: DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,418
FILING DATE: 17-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/270,013
FILING DATE: 01-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 164701/1993
FILING DATE: 02-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Allen E.
REGISTRATION NUMBER: 37354
REFERENCE/DOCKET NUMBER: 78339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: (25)3533
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-418-2

Query Match 41.8%; Score 706; DB 1; Length 329;
Best Local Similarity 45.3%; Pred. No. 1,7e-69;
Matches 136; Conservative 64; Mismatches 88; Indels 12; Gaps 3;
OY 9 RPKIMVSGMIGTMAFLCSLRELDVVLFDV--VPNNPMGRKAMDISHNSVDTGIV 66
Db 5 RKISIVIGAGFGATTAFLAOKELGDVVLVDIPELENTKGAIDMLLEASVYLGDAI 64
OY 67 YGSNSELKGDVYITAGIKIKIGSKSPKSRMDLFPVNIKIMEVGAIKSYCPNAF 126
Db 65 IGTSDYADTADSDIVVITAGIARKPG-----MSRDLVYTNOKIMQVTKYEVKKSPNCY 119
OY 127 VINTNPDLVVAALQESSGLPHHRICGMAGMLDSSRFRMTADKEVSPROVQGVICV 186
Db 120 IIVLINPDAIITYYFKESGPFKNRYIGOSGLVDTAREFTVAEELINISVKDVTGVLGG 179

OY 187 HDHNPVLSRATVNGIPLSEFVKKMIKOEVDIVOKTVAGGEIVRLIGGSAIYAP 246
Db 180 HGDMVPLVRSYAGIPILEKTIIPK-----DRDAIVERTKGGGEIYNLNGNSAYIAP 234
OY 247 GASAIOMAESEILKRRKRVMSCTILOGOYQVONHYLGPVCIYGRGVKRIIELELTAOR 306
Db 235 AASLIVENEAELIKDORILPAIAYLEGEYEGYIGVPTILGNGIEKVEIELELTEEK 294

RESULT 5

US-08-748-068-3
Sequence 3, Application US/08748068
Patent No. 5770410
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Chiral Synthesis
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,068
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,959
FILING DATE: 05-OCT-1994
APPLICATION NUMBER: GB 92 02033.8
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 04702.6
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 93/00204
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: (15-16)
OTHER INFORMATION: /note= "numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (28-29)
OTHER INFORMATION: /note= "numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (29-30)
OTHER INFORMATION: /note= "numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (30-31)
OTHER INFORMATION: /note= "numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (40-41)
OTHER INFORMATION: /note= "numbering discontinuity"
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NAME/KEY: Modified-site
LOCATION: (69-70)
OTHER INFORMATION: /note= "numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site

LOCATION: (73-74)
OTHER INFORMATION: /note= "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (83-84)
OTHER INFORMATION: /note= "- numbering discontinuity"
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NAME/KEY: Modified-site
LOCATION: (176-177)
OTHER INFORMATION: /note= "- numbering discontinuity"
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NAME/KEY: Modified-site
LOCATION: (181-182)
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FEATURE:
NAME/KEY: Modified-site
LOCATION: (196-197)
OTHER INFORMATION: /note= "- numbering discontinuity"
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NAME/KEY: Modified-site
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NAME/KEY: Modified-site
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OTHER INFORMATION: /note= "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (234-235)
OTHER INFORMATION: /note= "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (251-252)
OTHER INFORMATION: /note= "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (264-265)
OTHER INFORMATION: /note= "- numbering discontinuity"
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NAME/KEY: Modified-site
LOCATION: (286-287)
OTHER INFORMATION: /note= "- numbering discontinuity"
US-08-748-068-3

Query Match 24.4%; Score 412; DB 1; Length 317;
Best Local Similarity 28.1%; Pred. No. 3.9e-37;
Matches 89; Conservative 79; Mismatches 139; Indels 10; Caps 5;

QY 5 EKNTPRKIMVSGMIGMAFICSLRELG-D-VLFDVYPNMMKRAMDISHNSVVDIG 63
DB 2 KNGGARRVYVIGAGVGASVVALMNOGIADVLIDANESKAIIGAMDFNHGKVPAPK 61
QY 64 ITVGSNSYECLKGDVVTITAGITIKIPKSDKESRMDLPNIKIMREVGAIKSYCP 123
DB 62 VIMIGWDYDC-RDADIVYICAGANKPDE-----TRDLVKNKINIFSIYSVASGF 115
QY 124 NAFVINTNPDLVVAALQESSGLPHRIGCAGMLDSSRFRRMADKLEVSERDVGAV 183
DB 116 QGLFVATNPVILTYATKKFSGLPHERVYIGSGTIDTARFRFLGFEVSAPQNVHAYI 175
QY 184 IGWHGDHWPFLRYATVNGICPLSEPK-KGMIKQEEVDIVOKTKXVAGEIYVLLQGSN 242

DB 176 IGEHGTLELVWSQATYGVNPIKRVESKEENOKLERIFVNVDAVQIIE--KKGAT 233
QY 243 YVAGSAGIOMASYLEKDRKRVWVSCYLOGGVQNHLYGVPCVIGRGEVKIIELELT 302
DB 234 YVGIAMGLARVTRAILHNENAILVYSAYLDGIVGERVYIGVPAVINRNGIREVIEIEIN 293
QY 303 AQERQELQSIDYEKKEM 319
DB 294 DDEKNRFRHSAATLKSV 310

RESULT 6
US-08-748-068-1
Sequence 1, Application US/08748068.
Patent No. 5770410
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Chiral Synthesis
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,068
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,959
FILING DATE: 05-OCT-1994
APPLICATION NUMBER: GB 92 02033.8
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 04702.6
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 93/00204
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: (29-30)
OTHER INFORMATION: /note= "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (42-43)
OTHER INFORMATION: /note= "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (43-44)
OTHER INFORMATION: /note= "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (44-45)
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OTHER INFORMATION: /note= "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (83-84)
OTHER INFORMATION: /note= "- numbering discontinuity"

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FEATURE:
NAME/KEY: Modified-site
LOCATION: (87-88)
OTHER INFORMATION: /note- "- numbering discontinuity"
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NAME/KEY: Modified-site
LOCATION: (97-98)
OTHER INFORMATION: /note- "- numbering discontinuity"
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NAME/KEY: Modified-site
LOCATION: (195-196)
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FEATURE:
NAME/KEY: Modified-site
LOCATION: (210-211)
OTHER INFORMATION: /note- "- numbering discontinuity"
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NAME/KEY: Modified-site
LOCATION: (245-246)
OTHER INFORMATION: /note- "- numbering discontinuity"
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NAME/KEY: Modified-site
LOCATION: (249-250)
OTHER INFORMATION: /note- "- numbering discontinuity"
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NAME/KEY: Modified-site
LOCATION: (266-267)
OTHER INFORMATION: /note- "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (279-280)
OTHER INFORMATION: /note- "- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (302-303)
OTHER INFORMATION: /note- "- numbering discontinuity"
US-08-748-068-1
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Query Match 24.4% Score 412; DB 1; Length 333;
Best Local Similarity 29.9%; Pred. No. 4.2e-37;
Matches 101; Conservative 73; Mismatches 130; Indels 34; Gaps 10;

OY 5 EKNTRP-KIAMVSGMIGTMAFLCSLRELG-----DVLFDDVPPNPMGKAMDISHNSVDTGTT 57
DB 14 QETTPNKRITVGVGVGQV-----MACAISILKSLDELALVDLEKLGEMMDLQHS 69
OY 58 SVVDGIVVGSNTECLGADVITITAGITKIPGSKDESRMDLLPVNKKIRREGAA 117
DB 70 LFLQRP-KIVANKDYSVANSKIVVYTAGVROEGE-----SRLLVQNRVNVFKTIIPO 123
OY 118 IKSYPNPFVINITPLDVAALDESSGLPHHRICGAMGLDSSFRFMIADKLEVSFR 177
DB 124 IVKSPNCLIIIVSNPVDILTYVTWKLSGLPKHRVIGSGCNLDARSFRFLMAEKLCVHPS 183
OY 178 DVQGNVIGVGHMVPPLSRATVNGIPLSEF-----VKKGWIKOEVEDDIYOKTKYA 229
DB 184 SCHGILTEHGGSSVAVMSGVAVAGVSLQQLNPEKGTNDSENM--KEVHMKVVEASV- 239
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OY 230 GGEIVRLGGSAYVAPASAIOMAESYLKDRKRVWCSYLOGGYOVNH-YLGPCVI 288
DB 240 --EVKIL--KGYTNMAIGLSVADLIESMLKNSRHPSTWQMGYGIENEVFLSLPCVL 295
OY 289 GGRVEKIELETRPOEQLGSGIDEXKEMOKAIAL 326
DB 296 NARGLTSVINOKLADDEVAOLKNSADTLMGIQDKDL 333
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RESULT 7
US-08-869-506-2
Sequence 2, Application US/08869506
Patent No. 5827710
GENERAL INFORMATION:
APPLICANT: Uchida, Kohji
APPLICANT: Matsukawa, Hirokazu
APPLICANT: Matuo, Yushi
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
TITLE OF INVENTION: LACTATE DEHYDROGENASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 No. 5827710th Giebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,506
FILING DATE: 05-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 73797/1996
FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 159-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-869-506-2
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Query Match 23.2% Score 391; DB 2; Length 333;
Best Local Similarity 29.9%; Pred. No. 8.7e-35;
Matches 97; Conservative 69; Mismatches 138; Indels 20; Gaps 8;

OY 11 KIAMVSGMIGTMAFLCSLRELG-----DVLFDDVPPNPMGKAMDISHNSVDTGTT 65
DB 22 KITVGVGVGQV-----MACAISITGKGLCELAIVDLEKLGEMMDLQHSIFLQTH-K 76
OY 66 VYGSNTECLGADVITITAGITKIPGSKDESRMDLLPVNKKIRREGAAIKSCPN 125
DB 77 IVADQVAYTANSKIVVYTAGVROEGE-----SRLLVQNRVNVFKTIIPOIVKSPNC 131
OY 126 FVINITNPLDVAALDESSGLPHHRICGAMGLDSSFRFMIADKLEVSFRDVQGNVIG 185
DB 132 TLIVVSNPVDILTYVTWKLSGLPKHRVIGSGCNLDTARFRFLMAEKLGHPISCHMIIG 191
OY 186 VHGDMHVPPLSRATVNGIPLSEF-VKKGWIKOEVEDDIYOKTKVAGG-BIVRLGGGSAV 243
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Db 192 EHGDSVAWGVNNGVSLQELNPMAGTDKDENNKEVHKOVESAYEYIRL--KGYTN 249
QY 244 YAPGASAIQMAESYLKDRKRVWCSCYLOGQYGVONH-YLGVPCVIGRGVEKIIETELT 302
Db 250 WAIGLSVAELCETMLKNLYRVHSVSTLVKCTYGIENDVFLSLPCVLSASGLTSVINQK 309
QY 303 AOERQLOGSIDEVKEMOKAIAL 326
Db 310 DDEVQOLKRSADTLMSIQDKDL 333

RESULT 8

US-09-128-967-2
Sequence 2, Application US/09128967
Patent No. 6057141
GENERAL INFORMATION:
APPLICANT: Uchida, Kohji
APPLICANT: Matsukawa, Hirokazu
APPLICANT: Matuo, Yushi
APPLICANT: Fujita, Tutosi
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
LACTATE DEHYDROGENASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYTE P.C.
STREET: 1100 NO. 6057141th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/869,506
FILING DATE: 05-JUN-1997
APPLICATION NUMBER: JP 73797/1996
FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 159-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4000
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-128-967-2

Query Match 23.2%; Score 391; DB 3; Length 333;
Best Local Similarity 29.9%; Pred. No. 8,7e-35;
Matches 97; Conservative 69; Mismatches 138; Indels 20; Gaps 8.

QY 11 KIAMGSSMIGTMAFLCGLRELG-----DVLFLDYVPNMPMGKAMDISHNSVVDTGIT 65
Db 22 KITVGVGVGQV---MACAISILGKGLCDELALVLDLEDKLKGEMMDLQHGSLFLOTGTH-K 76
QY 66 VIGNSYELCKADAVYIYAGITKIPGKSDKESRMDLPVNIKIRIEVGAIAIKSYCPNA 125
Db 77 IYADNDYANTANSKIYVYTAGYRQDEGE-----SRNLVQRNVNVEKFIIPQIVKISPMC 131

QY 126 FVNIITNPDLVVAALQESSGLPHHRICGMAGLDSSRRFRMIADKLEVSPPRVQGVIG 185
Db 132 TILVSNPVDILYVWTKLSGLPKHRVYISGCNLDYRFRYLAEMERLGIHPTSCHGWIIG 191
QY 186 VGHDMWPLSRVNFVNCIPSEF-VKKGWIKQEEVDIVOKTVAGC-ELVRLLOGGSAY 243
Db 192 EHGDSVAWGVNNGVSLQELNPMAGTDKDENNKEVHKOVESAYEYIRL--KGYTN 249
QY 244 YAPGASAIQMAESYLKDRKRVWCSCYLOGQYGVONH-YLGVPCVIGRGVEKIIETELT 302
Db 250 WAIGLSVAELCETMLKNLYRVHSVSTLVKCTYGIENDVFLSLPCVLSASGLTSVINQK 309
QY 303 AOERQLOGSIDEVKEMOKAIAL 326
Db 310 DDEVQOLKRSADTLMSIQDKDL 333

RESULT 9

US-08-869-506-3
Sequence 3, Application US/08869506
Patent No. 5827710
GENERAL INFORMATION:
APPLICANT: Uchida, Kohji
APPLICANT: Matsukawa, Hirokazu
APPLICANT: Matuo, Yushi
APPLICANT: Fujita, Tutosi
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
LACTATE DEHYDROGENASE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYTE P.C.
STREET: 1100 NO. 5827710th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,506
FILING DATE: 05-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 73797/1996
FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 159-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4000
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-869-506-3

Query Match 23.1%; Score 380; DB 2; Length 333;
Best Local Similarity 29.6%; Pred. No. 1.1e-34;
Matches 96; Conservative 70; Mismatches 138; Indels 20; Gaps 8;

QY 11 KIAMGSSMIGTMAFLCGLRELG-----DVLFLDYVPNMPMGKAMDISHNSVVDTGIT 65
Db 22 KITVGVGVGQV---MACAISILGKGLCDELALVLDLEDKLKGEMMDLQHGSLFLOTGTH-K 76

QY 66 VYGSNSYECLGADVITITAGITKIPGSKDEKSMODLLPVNIKIMREVGAIKSYCNA 125
Db 77 IVADKDAVAVTANSKIYVYTAGVROEGE-----SRLNLYORNVNFKETIPIQIYKYSFNC 131
QY 126 FVINITPLDVMAALDOESSGLPHHRIGCMAGMLODSRFRMADKLEVSPPDVGWYIG 185
Db 132 VILVSNPVDILTYVTWMLKSLPKHRVYSGCNDLTARFRLMERLGIHPTSCGWILG 191
QY 186 VHGDHVPPLSRVATVNGIPLSEF-VKKGWIKOEVDIVQKTKVAGG-EIYRLGOGSAY 243
Db 192 EHGDSSVAWMSGVAVGVSILQOLDPAMGTDKDESMKKEVHNQVESAIVEAIRL--KGYTN 249
QY 244 YAPGASAIOMAESYLKDKRRVWVCSYLOGQYGVONH-YLGVPVYIGRGVEKIEILELT 302
Db 250 WAIGLSVAELCETMLKNIYRHVSSTLVKGTGIENDVFLSPCVLSASGLTSVYNOKLK 309
QY 303 AOEREOLOGSIDEVKEKOKAIAAL 326
Db 310 DDEVAOLKKSADTLMSIQDKDL 333

RESULT 10

US-09-128-967-3
Sequence 3, Application US/09128967
Patent No. 6057141
GENERAL INFORMATION:
APPLICANT: Uchida, Kohji
APPLICANT: Matsukawa, Hirokazu
APPLICANT: Matsumoto, Yushi
APPLICANT: Fujita, Tetsuji
TITLE OF INVENTION: DNA ENCODING THE SUBUNIT OF AVIAN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 No. 6057141th Giebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,967
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/869,506
FILING DATE: 05-JUN-1997
APPLICATION NUMBER: JP 73797/1996
FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 159-43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-128-967-3

Query Match 23.1%; Score 390; DB 3; Length 333;
Best Local Similarity 29.6%; Pred. No. 1,1e-34;

Matches 96; Conservative 70; Mismatches 138; Indels 20; Gaps 8;
QY 11 KIAMGSGMIGTMAFLCSLRELG-----DYLFPEYVNMFMGKAMDISHNSVVDIT 65
Db 22 KITVGVGVG---MACAISTLGLDELDALVDLBDKLGEMMDQHSLSFLQTH-K 76
QY 66 VYGSNSYECLGADVITITAGITKIPGSKDEKSMODLLPVNIKIMREVGAIKSYCNA 125
Db 77 IVADKDAVAVTANSKIYVYTAGVROEGE-----SRLNLYORNVNFKETIPIQIYKYSFNC 131
QY 126 FVINITPLDVMAALDOESSGLPHHRIGCMAGMLODSRFRMADKLEVSPPDVGWYIG 185
Db 132 VILVSNPVDILTYVTWMLKSLPKHRVYSGCNDLTARFRLMERLGIHPTSCGWILG 191
QY 186 VHGDHVPPLSRVATVNGIPLSEF-VKKGWIKOEVDIVQKTKVAGG-EIYRLGOGSAY 243
Db 192 EHGDSSVAWMSGVAVGVSILQOLDPAMGTDKDESMKKEVHNQVESAIVEAIRL--KGYTN 249
QY 244 YAPGASAIOMAESYLKDKRRVWVCSYLOGQYGVONH-YLGVPVYIGRGVEKIEILELT 302
Db 250 WAIGLSVAELCETMLKNIYRHVSSTLVKGTGIENDVFLSPCVLSASGLTSVYNOKLK 309
QY 303 AOEREOLOGSIDEVKEKOKAIAAL 326
Db 310 DDEVAOLKKSADTLMSIQDKDL 333

RESULT 11

US-08-748-068-2
Sequence 2, Application US/08748068
Patent No. 5770410
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Chiral Synthesis
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,068
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,959
FILING DATE: 05-OCT-1994
APPLICATION NUMBER: GB 92 02033.8
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 04702.6
FILING DATE: 04-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 93/00204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: (16-17)
OTHER INFORMATION: /note- --- numbering discontinuity"
FEATURE:
NAME/KEY: Modified-site
LOCATION: (27-28)
OTHER INFORMATION: /note- --- numbering discontinuity"

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Query Match          9.2% ; Score 155; DB 1; Length 327;
Best Local Similarity    24.3%; Pred. No. 8.3e-09;
Matches      83; Conservative   59; Mismatches 145; Indels   54; Gaps   17;;
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Db 6 RAAVTGAAGCGYSLPRLIAGCMLGKQPVIILOLEIPQAMKALEGVVMELEDCAPBL 65
 QY 62 TGTIVYSSNSECCKGADVITITGTRIKPEKSPKESRMDLPPVNIKIMEVGAIAIKSY 121
 Db 66 AGLEA-TDDRVAEKADADYAL---VGAAPKAGME--RRDLOVNGKIFPEGGALAEV 119
 QY 122 C-PRAFVINTNPLDV-MVALOESSCLPHRIGCMAGMDSSRRRIADKLEVSPPDV 179
 Db 120 AKDVKVLYVGNPANTNALLAYKNAPGLNPNFTAMT-RLDHNRKAQOLAKKTGTVDRI 178
 QY 180 QGNVI-GVHGDHMYPLSRVATVNGIPLSEFYKKGMIKOEVDLDVOKTVAGGEIVRLG 238
 Db 179 RRTVMGNHSTMPDLFHLAEVDSRPALELVDMEMEYKVFITYAQR---GAALIQARG 234
 QY 239 QGSATYAPGSAIQMAESYTKDKR-----RVWVCSCYLOGGVONHYLGPVCYIG 289
 Db 235 ASSA-----ASANAALAEHIDWALGTPEGDWVMAVPS---QGEYGIPEGIVYSFVTA 286
 QY 290 GRCVEKIE-----LELTAOROLOGSDIDEVKEK 319
 Db 287 KDCATRYVEGLEINERARKRMEITA---QELDMEQVKAL 324

RESULT 13

US-08-286-305A-3
 ; Sequence 3, Application US/08286305A
 ; Patent No. 5766863

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
 APPLICANT: Mark, Melanie R.
 APPLICANT: Sadick, Michael D.
 APPLICANT: Shelton, David L.
 APPLICANT: Wong, Wal Lee Tan
 TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: palin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,305A
 FILING DATE: 05-AUG-1994
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/170558
 FILING DATE: 20-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/157563
 FILING DATE: 23-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.

REGISTRATION NUMBER:

REGISTRATION NUMBER: 00,000
 REFERENCE/DOCKET NUMBER: 854C1P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO:

3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 814 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-286-305A-3

Query Match 5.2%; Score 87; DB 1; Length 814;
 Best Local Similarity 20.1%; Pred. No. 1.1;
 Matches 71; Conservative 36; Mismatches 83; Indels 164; Gaps 17;

QY 20 IGTMAFLCSLEIGADVLFDPVNPMPKAMDISHNSVVDGTITVYSGNSYECLEKAD 79
 Db 1 MGTAA-----RLGAVILFVVI-----VGLHGCVGKAL--AD 31
 QY 80 VVITAGTTRIPGSDKESRMDLPPVNIKIMEVGAIAISYCNAFVINTNPLDVVA 139
 Db 32 ASLMAADPNRRGKD-----LPVLDLLEVAAPCPDACCPHG----- 68
 QY 140 ALOESSCLPHRIGCMAGMDSSRF-----RRMIADKLEVSPPDVGM----- 182
 Db 69 -----SSGLR-----CTRGALDLSLHLGAEVLTLYENOQHLOHLEL--RDLSGLDEL 118
 QY 183 -----VIGVGHMPV-ISR-----YATVNGIPLSEFYKKG----- 212
 Db 119 NLTVKSGLRFVADAFHETPRLSRLMSFNALSLSKMTYOGSLQELVILSGNPLHCSC 178
 QY 213 -----WIKGEVDLDVOKTKVAGG---EIVRLGQGSATYAPGSAIQMAESYTKDKRVMV 266
 Db 179 ALRWLQWEEEGT-----GVPEQKLOCHGQGPLAHMNPASC----- 215
 QY 267 CSCYLOGGVONHYLGPV-----CVIGRGVEK-----IIELETA 303
 Db 216 -----GVPLTKGVPNASVDVGDVLLRCOVESRGLEQMGWILTELOS 260

RESULT 14

US-08-441-104A-3
 ; Sequence 3, Application US/08441104A
 ; Patent No. 5891650

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
 APPLICANT: Mark, Melanie R.
 APPLICANT: Sadick, Michael D.
 APPLICANT: Shelton, David L.
 APPLICANT: Wong, Wal Lee Tan
 TITLE OF INVENTION: KINASE RECEPTOR ACTIVATION ASSAY
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 720 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: palin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/441,104A
 FILING DATE: 15-MAY-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/286305
 FILING DATE: 05-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/170558
 FILING DATE: 20-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/157563
 FILING DATE: 23-NOV-1993
 ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER:

REGISTRATION NUMBER: 00,000
 REFERENCE/DOCKET NUMBER: 854C1P1C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 15, 2000, 09:46:44 : Search time 41.48 Seconds

(without alignments)
1078.393 Million cell updates/sec

Title: US-08-676-882-2

Perfect score: 1688

Sequence: 1 MAVREKMTNPRIAMVSGMT.....GSIDVEMKKAIALDASK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 870496 seqs, 135550690 residues

Total number of hits satisfying chosen parameters: 870496

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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27: /cgn2_6/ptodata/2/paa/US098.COMB.pep:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	828	49.1	315	1	PCT-US98-18626-2
2	828	49.1	315	4	US-08-046-160-2
3	828	49.1	315	6	US-08-024-594-2
4	828	49.1	315	14	US-08-932-194-2
5	828	49.1	315	14	US-08-932-194-2
6	706	41.8	329	13	US-08-838-418-2

7	641	38.0	325	18	US-09-450-969-7257	Sequence 7257, Ap
8	464	27.5	324	16	US-09-107-532-6486	Sequence 6486, Ap
9	426	25.2	318	16	US-09-134-000-4417	Sequence 4417, Ap
10	406	24.1	334	14	US-08-932-194-22	Sequence 22, Appl
11	406	24.1	334	27	US-60-238-331-75	Sequence 75, Appl
12	401.5	23.8	330	18	US-09-450-969-4667	Sequence 4667, Ap
13	400	23.7	331	14	US-08-932-194-23	Sequence 23, Appl
14	395.5	23.4	307	16	US-09-107-532-4274	Sequence 4274, Ap
15	395	23.4	330	14	US-08-932-194-21	Sequence 21, Appl
16	388	23.0	332	19	US-09-583-110-4591	Sequence 4591, Ap
17	384.5	22.8	338	13	US-08-827-356-3184	Sequence 3184, Ap
18	384.5	22.8	338	20	US-09-611-529-6846	Sequence 6846, Ap
19	371	22.0	381	21	US-60-212-664-505	Sequence 505, App
20	363	21.5	320	19	US-09-535-381-2	Sequence 2, Appl
21	362	21.4	332	21	US-60-167-217-21730	Sequence 21730, A
22	362	21.4	332	21	US-60-173-464-17678	Sequence 17678, A
23	362	21.4	332	21	US-60-191-637-21578	Sequence 21578, A
24	362	21.4	332	21	US-60-191-681-17015	Sequence 17015, A
25	356	21.1	381	17	US-09-215-435-443	Sequence 443, App
26	356	21.1	381	21	US-60-069-957-311	Sequence 311, App
27	353.5	20.9	351	21	US-60-191-637-30493	Sequence 30493, A
28	295	17.5	320	17	US-09-252-691-8059	Sequence 8059, Ap
29	284.5	16.9	336	21	US-60-167-217-17740	Sequence 17740, A
30	284.5	16.9	336	21	US-60-191-637-17738	Sequence 17738, A
31	279	16.5	312	27	US-60-215-161-7133	Sequence 7133, Ap
32	273.5	16.2	304	20	US-09-634-238-238	Sequence 238, App
33	260	15.4	347	21	US-60-167-324-2221	Sequence 2221, Ap
34	260	15.4	347	21	US-60-173-386-1981	Sequence 1981, Ap
35	260	15.4	347	21	US-60-175-871-2212	Sequence 2212, Ap
36	260	15.4	348	21	US-60-184-775-2026	Sequence 2026, Ap
37	257	15.2	347	21	US-60-191-637-42567	Sequence 42567, A
38	257	15.2	347	21	US-60-191-700-2151	Sequence 2151, Ap
39	246.5	14.6	338	14	US-08-922-957-11	Sequence 3, Appl
40	240	14.2	338	14	US-08-922-957-11	Sequence 11, Appl
41	238.5	14.1	338	16	US-09-160-911-11	Sequence 11, Appl
42	236.5	14.0	358	17	US-09-248-796-17253	Sequence 17253, A
43	236.5	14.0	358	21	US-60-096-409-17253	Sequence 17253, A
44	233	13.8	380	1	PCT-US00-05882-975	Sequence 975, App
45	231.5	13.7	298	14	US-08-922-957-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
PCT-US98-18626-2
Sequence 2, Application PC/TUS9818626
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING MALARIA
NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/18626
FILING DATE: 08 SEPTEMBER 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/932,194
FILING DATE: 17 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
NAME: REMILARD, JANE E.
REGISTRATION NUMBER: 38, 872
REFERENCE/DOCKET NUMBER: DCI-103PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2000, 09:46:44 ; Search time 23.01 Seconds

(without alignments)
1339.134 Million cell updates/sec

Title: US-08-676-882-2

Sequence: 1 MAVEKNTKRIAMVSGMI.....GSIDEVEMOKAIALDASK 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1041.5	61.7	329	5 P90613	P90613 toxoplasma
2	808.5	47.9	316	10 P93052	P93052 botryococcus
3	634	37.6	324	2 O55383	O55383 synechocyst
4	605.5	35.9	335	2 O67655	O67655 aquifex aeo
5	569	34.7	334	2 O67581	O67581 aquifex aeo
6	451	26.7	338	5 O44340	O44340 styela plic
7	440.5	26.1	353	10 O49191	O49191 arabidopsis
8	440.5	26.1	353	10 O23569	O23569 arabidopsis
9	430.5	25.5	331	13 O93537	O93537 harpagifer
10	428.5	25.4	331	13 O93545	O93545 lepidonotol
11	428	25.4	317	2 O59244	O59244 bacillus ca
12	427.5	25.3	331	13 O93541	O93541 champsoceph
13	426.5	25.3	331	13 O93549	O93549 chionodraco
14	424.5	25.1	331	13 O93546	O93546 patagonotot
15	423.5	25.1	331	13 O9PRR8	O9PRR8 notochenta
16	422.5	25.0	331	13 O93539	O93539 notochenta
17	422.5	25.0	331	13 O93540	O93540 globionototh
18	422	25.0	317	2 O9S0N0	O9S0N0 bacillus st
19	422	25.0	332	13 O93542	O93542 eleginops m

ALIGNMENTS

20	422	25.0	332	13 O9PW58	O9PW58 rhizophila
21	421.5	25.0	331	13 O93538	O93538 paracheanic
22	420	24.9	332	11 O64483	O64483 mus musculus
23	419.5	24.9	331	13 O93543	O93543 paraneotome
24	418	24.8	333	13 O9YGL2	O9YGL2 anguilla ro
25	415	24.6	332	13 O93401	O93401 coriophor
26	409.5	24.3	331	13 O93544	O93544 disostichu
27	409.5	24.3	331	13 O9PW61	O9PW61 disostichu
28	409	24.2	332	13 O93620	O93620 gillilichthys
29	407	24.1	332	13 O13276	O13276 sphyraena a
30	406	24.1	332	13 O13277	O13277 sphyraena a
31	406	24.0	332	13 O13278	O13278 sphyraena a
32	405.5	24.0	333	2 O32765	O32765 lactobacill
33	405	23.9	335	13 O9W7L4	O9W7L4 sceloporu
34	404	23.9	333	13 O9W7M6	O9W7M6 amylostoma m
35	404	23.9	334	13 O9PVK4	O9PVK4 brachydanio
36	404	23.8	333	10 O9ZKJ5	O9ZKJ5 oryza sativ
37	402	23.7	332	13 O9W5Z7	O9W5Z7 xenopus lae
38	400	23.7	332	6 O9XR87	O9XR87 monodelphis
39	400	23.7	334	6 O9YI05	O9YI05 squalus aca
40	400	23.7	350	10 O96569	O96569 lycopersico
41	399.5	23.7	350	10 O96569	O96569 lycopersico
42	399	23.6	331	13 O9PT42	O9PT42 trachemys s
43	399	23.6	333	13 O51114	O51114 borrelia bu
44	398	23.6	316	2 P79913	P79913 sceloporu
45	398	23.6	332	13	

RESULT 1					
ID	P90613	PRELIMINARY:	PRT:	329 AA.	
AC	P90613				
DT	01-MAY-1997 (TREMBL)	03, Created			
DT	01-MAY-1997 (TREMBL)	03, Last sequence update			
DT	01-MAY-2000 (TREMBL)	13, Last annotation update			
DE	LACTATE DEHYDROGENASE (EC 1.1.1.27) (L-LACTATE DEHYDROGENASE)				
DE	(LACTIC ACID DEHYDROGENASE)				
OS	Toxoplasma gondii.				
OC	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;				
OC	Toxoplasma.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-ME49;				
RX	MEDLINE: 97169139.				
RA	Yang S., Parmley S.F.;				
RT	"Toxoplasma gondii expresses two distinct lactate dehydrogenase				
RT	homologous genes during its life cycle in intermediate hosts.";				
RL	Gene 184:1-12(1997).				
CC	-I- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) = PYRUVATE + NADH.				
DR	EMBL: U35118; AAC47443.1;				
DR	HSSP: Q27743; ICET.				
DR	INTERPRO: IPR001236;				
DR	INTERPRO: IPR001557;				
DR	PFAM: PF000056; 1dh; 1.				
DR	PRINTS: PR00086; LLDHRCNASE.				
KW	Oxidoreductase.				
SO	SEQUENCE 329 AA; 35548 MW; F06387B5AC0E6BBB CRC64;				
Query Match	61.7%	Score 1041.5;	DB 5;	Length 329;	
Best Local Similarity	60.4%	Pred. No. 3.3e-72;			
Matches 194;	Conservative 55;	Mismatches 71;	Indels 1;	Gaps 1;	
OY	9 RKRIAMVSGMIGTMAPLCSRELADVLLFPVVPMPKGMKAMDISHNSVVDGTYVG 68				
DB	9 RKKVAMIGSMIGTMGYCALRELADVLLDYVKGMPKGLDLSHVSYVDVNSVRA 68				
OY	69 SWSYE-CLKGADVVIITGITKIPKSDKESRMDLLPVNITIMEVGAIISYCPNAFV 127				
DB	69 EYSYEAALGACDVIVTGLTKVPKPSSEWSRNDLLPENSKITIREIGNIKKYCPKTFI 128				

OY 299 LELTAEROLOGSIDEVEMOKAI 323
 Db 305 MTLKAEEROKLOKSATLNGVOKEL 329

RESULT 11

059244 PRELIMINARY: PRT: 317 AA.
 AC 059244:
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE L-LACTATE DEHYDROGENASE (EC 1.1.1.27).
 OS Bacillus caldolyticus.
 OC Bacteria, Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 88050101.
 RX Zuehl F., Weber H., Zuber H.;
 "Structure and function of L-lactate dehydrogenases from thermophilic
 RT and mesophilic bacteria, VI. Nucleotide sequences of lactate
 RT dehydrogenase genes from the thermophilic bacterium Bacillus
 RT stearothermophilus, B. caldolyticus and B. caldolenax.";
 RL Biol. Chem. Hoppe-Seyler 368:1167-1177(1987).
 CC -1- CATALYTIC ACTIVITY: L-LACTATE + NAD(+) -> PYRUVATE + NADH.
 CC -1- SUBUNIT: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 DR EMBL: M19394; AAA22564.1;
 DR HSSP: P00344; 1LDH.
 DR INTERPRO: IPR000205;
 DR INTERPRO: IPR000594;
 DR INTERPRO: IPR00136;
 DR INTERPRO: IPR001557;
 DR PFM: PF00056; 1dh; 1.
 DR PRINTS: PR00086; LLDHRCNASE.
 DR PROSITE: PS00064; L.LDH; 1.
 DR Oxidoreductase; NAD: Glycolysis.
 FT ACT SITE 179
 SQ SEQUENCE 317 AA: 34818 MW; 7A1D85428B0C0E8 CRC64;

Query Match 25.4%; Score 428; DB 2; Length 317;

Best Local Similarity 29.0%; Pred. No. 3.6e-25;
 Matches 92; Conservative 77; Mismatches 138; Indels 10; Gaps 5;

OY 5 EKNTKRIAMVSGMIGTMAFLCSLRELGD-VLFEDVVPNNPKAMDISHNSVVDTG 63
 Db 2 KNGGTRVYVIGTGVGASATFALMNOGIADLVLIDANESAIIGDAMPNNGKVPAPRP 61
 OY 64 ITVYSNSTECKAGADVITTAGITRIKIPKSDKEMSRMDLFPVNIRKIMEVGAIAKSYCP 123
 Db 62 ADIMHGDDYDC-RDADLVVYICAGANOKPGE-----TRLDLVKNIAIFRSIVESVASGF 115
 OY 124 NAFVINITPPLDVMAALQESSGLPHHRIICGAMGLDSSRFRRMADKLEVSPPDVQNAV 183
 Db 116 OGELFVATNPVILTYLVWKFSGLPHRYIGSGTLLDVARFPLLGGEYSPAPNVHAYI 175
 OY 184 IGVHSDHMPLSRYATVNGIPLSEFVK-KGMIKOEVDIVQTKVAGEIVRLGOGSA 242
 Db 176 IGEHGDTELPRVMSQADIGVPIRKLIVESGEAKKELEIFPVNDAQIIE-KKQAT 233
 OY 243 YIAPASAIOMAESYLKDRKRVWVCYLOGOYGVQNHVLPVCYIGRGVEKITELELT 302
 Db 234 YYGIMAGLARVTRALIHENAILTVSAVLDGPGERDVYIGVPAYINRNGIREVIEIENL 293
 OY 303 AEROLOGSIDEVEMOKAI 319
 Db 294 DDEKNRPHHSATLKS 310

RESULT 12

093541

ID 093541 PRELIMINARY: PRT: 331 AA.
 AC 093541:
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE LACTATE DEHYDROGENASE-A (EC 1.1.1.27).
 CN LDH-A.
 OS Champsocephalus gunnari.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
 OC Percormorpha; Perciformes; Notothenioidei; Channichthyidae;
 OC Champsocephalus.
 RN (1)
 RP SEQUENCE FROM N.A.
 RA TISSUE=MUSCLE;
 RC Fields P.A., Somero G.N.;
 "Hot spots in cold adaptation: lactate dehydrogenase-A (A4-LDH)
 RT orthologs of antarctic notothenioid fishes.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF079824; AAC63282.1;
 DR HSSP: P00336; 5LDH.
 DR INTERPRO: IPR001236;
 DR INTERPRO: IPR001557;
 DR PFM: PF00056; 1dh; 1.
 DR PRINTS: PR00086; LLDHRCNASE.
 DR PROSITE: PS00064; L.LDH; 1.
 DR Oxidoreductase.
 SQ SEQUENCE 331 AA: 36156 MW; 556546DC3A03237E CRC64;

Query Match 25.3%; Score 427.5; DB 13; Length 331;

Best Local Similarity 31.4%; Pred. No. 4.1e-25;
 Matches 103; Conservative 68; Mismatches 128; Indels 29; Gaps 8;

OY 8 TRPKIAMVSGMIGTMAFLCSLRELGD-VLFEDVVPNNPKAMDISHNSVVDTG 66
 Db 19 SKKVTVGAGVGVASATLILKDLCDLAMDVEDLKGVDLQSGSFLKTKIY 77
 OY 67 YGSNSTECKAGADVITTAGITRIKIPKSDKEMSRMDLFPVNIRKIMEVGAIAKSYCP 126
 Db 78 -GDKDSVTANSKVVVVTAGARQEGE-----SRLLVORNVNITKFTIPNIVKISPNCT 131
 OY 127 VINITPPLDVMAALQESSGLPHHRIICGAMGLDSSRFRRMADKLEVSPPDVQNAV 186
 Db 132 LMVSNPVDILTYLVWKLSGFPFRHYIGSGTLLDVARFPLLGGEYSPAPNVHAYI 191
 OY 187 HDHMPLSRYATVNGIPL-----SEFVKGM--IKOEVDIVQTKVAGEIVRL 236
 Db 192 HGDSSVPVMSGVNAGVSLQGLNPOMGTGDEGNMKAIRKEVVD-----GAVEVIL 243
 OY 237 LGGSAVYVAPGASAIOMAESYLKDRKRVWVCYLOGOYGVQNH-VLGPVCYIGRGVEK 295
 Db 244 KGYTS--WAIQMSVADLVESITIKNMHKAHPVSTLVQGMHGRDEVFLSVPCVLTGNSGLTD 301
 OY 296 IIELELTAEEROKLOKSATLNGVOKEL 323
 Db 302 VIHMTLKAEEEROKLOKSATLNGVOKEL 329

RESULT 13

093619

ID 093619 PRELIMINARY: PRT: 331 AA.
 AC 093619:
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE LACTATE DEHYDROGENASE-A (EC 1.1.1.27).
 CN LDH-A.
 OS Chionodraco rastrospinosus, Chaenocephalus aceratus, and
 OS Trematomus bernacchii.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
 OC Percormorpha; Perciformes; Notothenioidei; Channichthyidae;

Query Match	25.1%	Score 424.5;	DB 13;	Length 331;
Best Local Similarity	31.1%	Pred. No. 7e-25;		
Matches 102;	Conservative 69;	Mismatches 128;	Indels 29;	Gaps 8;
QY	8	TRPKIAMSSGIMGIMAFGLCSLRELGD-VLFQVPPNPKGKAMDISHNSVVDPTGV	66	
DB	19	SSKSTVVGIVGVGNASASLILKDCODELAVDVDEKLGEVVDLQIGSLFLKTKIV	77	
QY	67	YGSNSYECCAGADVITPAGITKICKOKSEKMSRBDLLPVNKKIREVGAALIKSCPNAF	126	
DB	78	-CDKDYSTVANSKVVVYVYTAGAQOEE-----SLNLVQRNVNIFKFIIPNIVKTSPTCI	131	
QY	127	VINTNPDLDMVALAEOESSGLPRHNRICGMAGMIDSSRFRRITADKLEVPDVGGMVIGV	186	
DB	133	LMVNSNPVDILTYVMKLKSGFPRHNVIGSGTFLDARFRHLGKELHLHPSCHAMTYGE	191	
QY	187	HDDHNVPLSRATVNGVPL-----SEFVKKGM--IKOEEVDDIYOKTKVAGEIYRL	236	
DB	192	HDDSSVPVSGVGNVAGVSLQGLNIPQMGTGEDENMKAIHKEVVD-----GAVEVTKL	243	
QY	237	IGGAGVAYVARGASALOMAESYLDKDRKRWVWCSCTGCGOYGVGNH-YLGVPCTGGRGVK	295	
DB	244	KGYTS--WALGMSVADLVESITIKNNHKHNPVSTLVQGMHGVKDEVLSVPCVLGNSGLTD	301	
QY	296	IIELRLAEROELGSGIDEVKEKOKAI 323		
DB	302	VTHMTLKAEEKQVOKSAETLMGVOKEL 329		
RESULT 15				
Q9PRH8	PRELIMINARY;	PRT;	331 AA.	
AC	Q9PRH8			
DT	01-MAY-2000 (TREMBLREL. 13, Created)			
DT	01-MAY-2000 (TREMBLREL. 13, Last sequence update)			
DT	01-JUN-2000 (TREMBLREL. 14, Last annotation update)			
DE	LACTASE DEHYDROGENASE-A (EC 1.1.1.27).			
GN	LDH-A.			
OS	Notothenia angustata (Rockcod), and			
OS	Parotthenia boreogrevinkii (Bald rockcod) (Trematomus boreogrevinkii).			
OC	Euthariota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;			
OC	Percomorpha; Perciformes; Notothenioidae; Nototheniidae; Notothenia.			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-WHITE MUSCLE;			
RA	Marshall C.J., Fleming R.I.;			
RT	"Cold adaptation in lactate dehydrogenases from antarctic fish."			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF170846; AAD48488.1;			
DR	EMBL: AF170846; AAD48486.1;			
DR	INTERPRO: IPR001236;			
DR	INTERPRO: IPR001557;			
DR	PFAM: PF00056; LDH; 1.			
DR	PRINTS: PRO0086; LLDHRCGNASE.			
DR	PROSITE: PS00064; L_LDH; 1.			
KW	PROSITE, PS00064; L_LDH; 1.			
Q0	SEQUENCE 331 AA; 36169 MW; 7CB80409CAQDAE9 CRC64;			

00339 sus scrofa
42120 xenopus lae
55611 lactobacill
29563 vulpes vulp
42121 xenopus lae
008349 archaeoglob
P196229 rattus norv
P16125 mus musculu
P421123 rattus norv
P19858 bos taurus
P04642 rattus norv
G92055 fundulus he

ALIGNMENTS

330 KALDASKAIA EMORE

STANDARD;	PRT;	326 AA.
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326 AA.

326 AA.

326 AA.

326 AA.

326 AA.

326 AA.

326 AA.

326 AA.

326 AA.

326 AA.

[illegible]

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EMBL: U23207; AAC46863.1;
HSSP: Q27743; LLDG.
INTERPRO: IPR001236;
INTERPRO: IPR001557;
PFAM: PF00056; LDH; 1.
PRINTS: PR00086; LLDHDEGNASE.
PROSITE: PS00064; L.LDH: FALSE NEG.
Oxidoreductase: NAD; Glycolysis
ACT_SITE 186 186
ACCEPTS A PROTON DURING CATALYSIS
(bY SIMILARITY)
E692C95A81FC031E CRC64:
SEQUENCE 326 AA: 35307 MW:
-----
DB 1: Length 326:

```

Query Match	Similarity	Best local Matches	Score	Pred. No.	Indels	Gaps
Match 199; Conservative	63.5%; 62.6%	56	1.5e-74;	63;	0;	

[illegible]

RESULT 2
 MDH_RHILV
 ID MDH_RHILV STANDARD: PRT: 320 AA.
 AC 033525;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE MALATE DEHYDROGENASE (EC 1.1.1.37).
 GN MALATE DEHYDROGENASE (EC 1.1.1.37).
 OS Rhizobium leguminosarum (biovar viciae).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group.
 RN Rhizobiaceae; Rhizobium.
 RC
 RP SEQUENCE FROM N.A.
 RA STRAIN-3841;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) -> OXALOACETATE + NADH.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: AJ002750; CA05717.1;
 DR HSP: 027743; 1LDG;
 DR INTERPRO: IPR001236;
 DR INTERPRO: IPR001252;
 DR INTERPRO: IPR001557;
 DR PFAM: PF00056; 1dh; 1.
 DR PRINTS: PR00066; LLDHRCNASE.
 DR PROSITE: PS00068; MDH; FALSE_NEG.
 DR OXIDOREDUCTASE: Tricarboxylic acid cycle; NEG.
 FT ACT_SITE 149 149 PROTON RELAY (BY SIMILARITY).
 FT BINDING 152 152 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
 FT ACT_SITE 176 176 PROTON-RELAY (BY SIMILARITY).
 SO SEQUENCE 320 AA; 33590 MW; 2094407442CB18 CRC64;
 Query Match 52.5%; Score 886.5; DB 1; Length 320;
 Matches 171; Conservative 59; Mismatches 79; Indels 5; Gaps 1;
 QY 9 RKIMAVGSGMTAFELCSRLKGLVLPVYVNMGRKAMDISHNSSVYDTITVYG 68
 DB 3 RNMKALISSGMIGTGLHLAGLKEGLDVLIDIDGIPQGGKGLDIOSSPVEGFDVNLG 62
 OY 69 SNSYECKGADVVIITAGITIKPKSKDKMSRMDLVPNPKIMRVEGAATKSYCPNPFVI 128
 DB 63 ASDSAIEAGDVCIVTAGVAKRG-----MSRDLLGILNKLKVMEOVGAGIKKTAPNPFVI 117

RESULT 3
 LDH1_PLAFD
 ID LDH1_PLAFD STANDARD: PRT: 316 AA.
 AC 027743;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1997 (Rel. 35, Last sequence update)
 DE L-LACTATE DEHYDROGENASE (EC 1.1.1.27) (LDH-P).
 OS Plasmodium falciparum (isolate CDC / Honduras).
 GN Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 RN Plasmodium falciparum (isolate CDC / Honduras).
 RC
 RP SEQUENCE FROM N.A.
 RA STRAIN-HONDURAS 1;
 RL MEDLINE: 93295434.
 RA Bzik D.J., Fox B.A., Gonyer K.;
 RT Expression of Plasmodium falciparum lactate dehydrogenase in
 RT Mol. Biochem. Parasitol. 59:155-166(1993).
 RL [2]
 RA X-RAY CRYSTALLOGRAPHY (1.74 ANGSTROMS).
 RA Dunn C., Banfield M., Barker J., Higham C., Moreton K.,
 RA Turgut-Balik D., Brady L., Holbrook J.J.,
 RT The structure of lactate dehydrogenase from Plasmodium falciparum
 RT reveals a new target for anti-malarial design.
 RL Nat. Struct. Biol. 3:912-915(1996).
 CC -1- CATALYTIC ACTIVITY: L-LACTATE + NAD(+) -> PYRUVATE + NADH.
 CC -1- SUBUNIT: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
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 DR EMBL: M93720; AAA29633.1;
 DR PDB: 1LDG; 17-SEP-97.
 DR PDB: 1CRO; 19-MAR-99.
 DR PDB: 1CET; 19-MAR-99.
 DR INTERPRO: IPR001236;
 DR INTERPRO: IPR001557;
 DR PFAM: PF00056; 1dh; 1.
 DR PRINTS: PR00066; LLDHRCNASE.
 DR PROSITE: PS00064; L-LDH; FALSE_NEG.
 DR OXIDOREDUCTASE: NAD; Glycolysis; 3d-structure.
 FT ACT_SITE 182 182 ACCEPTS A PROTON DURING CATALYSIS
 FT VARIANT 73 73 A -> S.
 FT VARIANT 96 96 D -> L.
 SO SEQUENCE 316 AA; 34108 MW; D25EB863954B8FC1 CRC64;
 Query Match 49.3%; Score 831.5; DB 1; Length 316;

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DR EMBL: 005257: AAA6343.1;
DR EMBL: AF008220: AAC00347.1;
DR EMBL: 299118: CAC14872.1;
DR HSSP: 027743: 1LDG;
DR SUBTILIST: BG11386; C17H;
DR INTERPRO: IPR001236;
DR INTERPRO: IPR001252;
DR INTERPRO: IPR001557;
PFAM: PF00056; 1dh; 1;
PRINTS: PR00086; LLDHRCNASE.
DR PROSITE: PS00068; MDH; FALSE; NEG.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT INIT_MET 0
FT ACT_SITE 152 152 PROTON-RELAY (BY SIMILARITY).
FT BINDING 155 155 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
FT ACT_SITE 179 179 PROTON-RELAY (BY SIMILARITY).
SQ SEQUENCE 311 AA; 33512 MW; 475287BFB852FB09 CRC64;

Query Match 43.8%; Score 740; DB 1; Length 311;
Best Local Similarity 45.9%; Pred. No. 2.5e-49;
Matches 147; Conservative 63; Mismatches 98; Indels 12; Gaps 3;

QY 7 NTRPKIAVWGSGMIGTAFGLCSLRELDGVLPDY--VPNMPGKAMDISHNSVVDGCI 64
DB 2 NTRKRVSYVIGAGFTGATTAFLAOKELADVIVDIPLENPKGALDMLKSPVQGEDA 61
QY 65 TVYGSNSYECLEKADGVITITAGITKIPKSDKESRMDLPVNIKIMREYGAIRKSPNAF 124
DB 62 KITGSNEYEDFAGSDIVITAGIARKPG-----MSRDLVOTNOKWAKSTKEVYKSPSI 116
QY 125 AFINITPLDVMVAALQESSGLPHIRICGMAGLDSSFRFRIADKLEVSPPDVQAGVI 184
DB 117 SIIVLTPVDMAITVAYKESGFPKRVIVIGSGVLDIARFRFVAEELNSVKDVTGFLV 176
QY 185 GVHGDHVPPLSRATVAVNGIPLSEFVKKGMIOKEEVDIYOKTVAGGEYIRLLGGSAIY 244
DB 177 GGHGDMVPLVRYSYAGCIPLLETLIPK-----ERIDAIYERTKKGGEIVNLGGSAYV 231
QY 245 APGASAIOMAESYLKDRKRVWVSCYLOGGVONHYLGPVCIYGGKVEKIIIELELTAQ 304
DB 232 APAASLTVEVAIIKDKORVLPJTAIVLEGEYEGYILGVPTIYGCNLEQIIIELELTDY 291
QY 305 EROELGSDIEVKEMOKAIA 324
DB 292 ERAOLNKSVESSVKVMKVL 311

RESULT 6
MDH_BACIS STANDARD: PRT: 312 AA.
AC 059202;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MALATE DEHYDROGENASE (EC 1.1.1.37).
GN MDH;
OS Bacillus israeli.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96276423.
RA Wayne S.A., Nicholls D.J., Scaven M.D., Sundaram T.K.;
RT "Tetrameric malate dehydrogenase from a thermophilic Bacillus:
cloning, sequence and overexpression of the gene encoding the enzyme
RT and isolation and characterization of the recombinant enzyme".
RL Biochem. J. 317:235-245(1996).

CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) = OXALOACETATE + NADH.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.

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DR EMBL: X90527: CAA62129.1;
DR HSSP: 027743: 1LDG;
DR INTERPRO: IPR001236;
DR INTERPRO: IPR001252;
DR INTERPRO: IPR001557;
PFAM: PF00056; 1dh; 1;
PRINTS: PR00086; LLDHRCNASE.
DR PROSITE: PS00068; MDH; FALSE; NEG.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT ACT_SITE 153 153 PROTON-RELAY (BY SIMILARITY).
FT BINDING 156 156 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
FT ACT_SITE 180 180 PROTON-RELAY (BY SIMILARITY).
SQ SEQUENCE 312 AA; 33648 MW; 64CE3BFF1B3C02D2 CRC64;

Query Match 43.2%; Score 729; DB 1; Length 312;
Best Local Similarity 44.5%; Pred. No. 1.7e-48;
Matches 141; Conservative 69; Mismatches 95; Indels 12; Gaps 3;

QY 9 RPKIAVWGSGMIGTAFGLCSLRELDGVLPDY--VPNMPGKAMDISHNSVVDGCI 66
DB 5 RKRIVIGAGFTGATTAFLAOKELADVIVDIPLENPKGALDMLKSPVQGEDA 64
QY 67 YGSNSYECLEKADGVITITAGITKIPKSDKESRMDLPVNIKIMREYGAIRKSPNAF 126
DB 65 IGTSEYEEFADSDIVITAGIARKPG-----MSRDLVOTNOKWAKSTKEVYKSPSI 119
QY 127 VINTNPLDVMVAALQESSGLPHIRICGMAGLDSSFRFRIADKLEVSPPDVQAGVI 186
DB 120 IIVLTPVDMAITVAYKESGFPKRVIVIGSGVLDIARFRFVAEELNSVKDVTGFLV 179
QY 187 HGDHVPPLSRATVAVNGIPLSEFVKKGMIOKEEVDIYOKTVAGGEYIRLLGGSAIY 246
DB 180 HGDDHVPPLVRYSYAGCIPLLETLIPK-----ERLEAIYERTKKGGEIVNLGGSAYV 234
QY 247 GASAIOMAESYLKDRKRVWVSCYLOGGVONHYLGPVCIYGGKVEKIIIELELTAQ 306
DB 235 AASLTVEVAIIKDKORVLPJTAIVLEGEYEGYILGVPTIYGCNLEQIIIELELTDY 294
QY 307 OELOGSDIEVKEMOKAI 323
DB 295 AALEKSAESVVRVMKAL 311

RESULT 7
MDH_BACIC STANDARD: PRT: 312 AA.
AC 09X4K8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MALATE DEHYDROGENASE (EC 1.1.1.37).
GN MDH;
OS Bacillus thermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=00462;
RA Williams R.A.D., Welch S.G., Alawadhi S.A.;
RT "Properties and primary structure of a thermostable L-malate

```

RT dehydrogenase from 'Bacillus thermocellulosus';
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) -> OXALOACETATE + NADH.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
CC
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CC EMBL: AF114423; AAD2855.1;
CC INTERPRO: IPR001236;
CC INTERPRO: IPR001252;
CC INTERPRO: IPR001557;
CC PFAM: PF00056; 1dh; 1.
CC PRINTS: PR00086; MDH; FALSE_NEG.
CC PROSITE: PS00068; MDH; FALSE_NEG.
CC Oxidoreductase; Tricarboxylic acid cycle; NAD.
CC ACT_SITE 153 153 PROTON-RELAY (BY SIMILARITY).
CC BINDING 156 156 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
CC ACT_SITE 180 180 PROTON-RELAY (BY SIMILARITY).
CC SEQUENCE 312 AA; 33682 MW; 68C691C462EFP452 CRC64;

Query Match 42.4%; Score 715; DB 1; Length 312;
Best Local Similarity 43.5%; Pred. No. 2e-47;
Matches 138; Conservative 69; Mismatches 98; Indels 12; Gaps 3;

OY 9 RPIIAWGSGMIGCTMAFLCSLRELDVLFV--VPNPMGKAMDISHNSVVDGTITV 66
DB 5 RKIIIVGFGTATTAFLAOKELDIVLVDIPOLNPTKALMLLESSPVLGSDANI 64
OY 67 YGSNSYECKGADVITITGTRIKPKSKDEMSRMDLIPNIMKEVGAIKSYCPNAP 126
DB 65 VGSODVADPADSDIVITITGTRIKPKSKDEMSRMDLIPNIMKEVGAIKSYCPNAP 126
OY 127 VNITNPLDVVAALQESSGLPHHRICGMAGMLDSRFRMIMADKLEVSPPDVGAVIG 186
DB 120 IIVLTNPVDMASYTFVKEGSPFKNRVITGSGVLDTRFRFTVAQELINISKVDTGVLGG 179
OY 187 HGDHWPPLSRATVNCIPLESEFVKKGMKIQEYVDIVQTKYAGGIVRLGGSGAYAP 246
DB 180 HGDHWPPLSRATVNCIPLESEFVKKGMKIQEYVDIVQTKYAGGIVRLGGSGAYAP 246
OY 247 GASAIOMAESYTKDKRRVWVSCYLOGGYVGNHNYGVCVIGRGVEKITELETAQER 306
DB 235 AASLAEWFAIVKDKRRILPAITYLEGEGYEGYIVLPITLIGNGIEKVIETELTEDEK 294
OY 307 QELGSDIEVKEMOKAI 323
DB 295 AALAKSLESVKVMRYL 311

RESULT 8
MDH_CHLAU
ID MDH_CHLAU STANDARD: PRT: 309 AA.
AC P80040:
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence, update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE MALATE DEHYDROGENASE (EC 1.1.1.37).
GN MDH.
OS Chloroflexus aurantiacus.
OC Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;
OC Chloroflexaceae; Chloroflexus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-J-10-FL;
RX MEDLINE: 96241868.
RA Synstad B., Emmertthoff O., Sirevag R.;

```

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RT Malate dehydrogenase from the green gliding bacterium Chloroflexus
RT aurantiacus is phylogenetically related to lactic dehydrogenases.*;
RL Arch. Microbiol. 165:346-353(1996).
CC [2]
CC SEQUENCE OF 1-35.
CC STRAIN-J-10-FL;
CC MEDLINE: 88257004.
CC Rolstad A.K., Howland E., Sirevag R.;
CC "Malate dehydrogenase from the thermophilic green bacterium
CC Chloroflexus aurantiacus: purification, molecular weight, amino acid
CC composition, and partial amino acid sequence.*";
CC J. Bacteriol. 170:2947-2953(1988).
CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) -> OXALOACETATE + NADH.
CC -1- SUBUNIT: HOMOTETRAMER (ACTIVE ENZYME); HOMODIMER AND HOMOTRIMER
CC AT TEMPERATURES LOWER THAN 55 DEGREES CELSIUS (INACTIVE FORMS).
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
CC
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CC
CC EMBL: X89038; CA61436.1;
CC HSP: Q27743; 1LDG.
CC INTERPRO: IPR001236;
CC INTERPRO: IPR001252;
CC INTERPRO: IPR001557;
CC PFAM: PF00056; 1dh; 1.
CC PRINTS: PR00086; MDH; FALSE_NEG.
CC PROSITE: PS00068; MDH; FALSE_NEG.
CC Oxidoreductase; Tricarboxylic acid cycle; NAD.
CC ACT_SITE 148 148 PROTON-RELAY (BY SIMILARITY).
CC BINDING 151 151 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
CC ACT_SITE 175 175 PROTON-RELAY (BY SIMILARITY).
CC SEQUENCE 309 AA; 32717 MW; 97743CC07F3F35 CRC64;

Query Match 40.0%; Score 676; DB 1; Length 309;
Best Local Similarity 43.8%; Pred. No. 1.8e-44;
Matches 141; Conservative 55; Mismatches 110; Indels 16; Gaps 3;

OY 9 RPIIAWGSGMIGCTMAFLCSLRELDVLFVVPNPMGKAMDISHNSVVDGTITV 68
DB 2 RKIIIVGFGTATTAFLAOKELDIVLVDIPOLNPTKALMLLESSPVLGSDANI 64
OY 69 SNEYELCKGADVITITGTRIKPKSKDEMSRMDLIPNIMKEVGAIKSYCPNAP 128
DB 62 TNNYADTANSDIVITITGTRIKPKSKDEMSRMDLIPNIMKEVGAIKSYCPNAP 128
OY 129 NITNPLDVVAALQESSGLPHHRICGMAGMLDSRFRMIMADKLEVSPPDVGAVIG 188
DB 117 MWNPLDAMFTYLAESVSGPKRNVITGSGVLDTRFRFTVAQELINISKVDTGVLGG 176
OY 189 DHMWPPLSRATVNCIPLESEFVKKGMKIQEYVDIVQTKYAGGIVRLGGSGAYAP 248
DB 177 DHMWPPLSRATVNCIPLESEFVKKGMKIQEYVDIVQTKYAGGIVRLGGSGAYAP 248
OY 249 SALOMAESYTKDKRRVWVSCYLOGGYVGNHNYGVCVIGRGVEKITELETAQER 308
DB 232 ATRQWAEVAVLKDKRRVWVSCYLOGGYVGNHNYGVCVIGRGVEKITELETAQER 308
OY 309 LOGSIDEVEMOKAIALDASK 330
DB 292 LMAAKAVR-----ATLDTLK 307

RESULT 9
MDH_CHLITE
ID MDH_CHLITE STANDARD: PRT: 310 AA.
AC P80039; P94677;

```



```

OC Bacillus/Staphylococcus group: Bacillus.
RN [1]
RE SEQUENCE FROM N.A.
RX MEDLINE: 90241471.
RA Vckovski V., Schlatter D., Zuber H.;
RT "Structure and function of L-lactate dehydrogenases from
RT thermophilic, mesophilic and psychrophilic bacteria, IX.
RT identification, isolation and nucleotide sequence of two L-lactate
RT dehydrogenase genes of the psychrophilic bacterium Bacillus
RT psychrosaccharolyticus."
RL Biol. Chem. Hoppe-Seyler 371:103-110(1990).
RN [2]
RP SEQUENCE.
RX MEDLINE: 86134573.
RA Schlatter D., Kriech O., Suter F., Zuber H.;
RT "The primary structure of the psychrophilic lactate dehydrogenase
RT from Bacillus psychrosaccharolyticus."
RL Biol. Chem. Hoppe-Seyler 368:1435-1446(1987).
CC -1- CATALYTIC ACTIVITY: L-LACTATE + NAD(+) -> PYRUVATE + NADH.
CC -1- PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
CC -1- SUBUNIT: HOMOTETRAMER.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X55118; CAA38914.1;
CC PIR: S08182; S08182.
CC HSSP: P00344; 1LDB.
CC INTERPRO: IPR001236;
CC INTERPRO: IPR001557;
CC PFAM: PF00056; 1dh; 1.
CC PRINTS: PR00086; LLDHRCNASE.
CC PROSITE: PS00064; L_LDH; 1.
CC Oxidoreductase; NAD: Glycolysis; Multigene family.
CC ACT_SITE 179 179 BY SIMILARITY.
CC FT ACT_SITE 179 179
CC SEQUENCE 318 AA: 35249 MW: F69165A3408E442A CRC64;

Query Match 26.1%; Score 440; DB 1; Length 318;
Best Local Similarity 30.6%; Pred. No. 1.6e-26;
Matches 96; Conservative 80; Mismatches 122; Indels 16; Gaps 7;

```

```

LDH_THEMA
ID LDH_THEMA STANDARD: PRT: 319 AA.
AC P16115:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE L-LACTATE DEHYDROGENASE (EC 1.1.1.27).
GN LDH OR TMI867.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-MSB8 / DSM 3109;
RX MEDLINE: 94009031.
RA Ostendorp R., Liebl W., Schurig H., Jaenicke R.;
RT "The L-lactate dehydrogenase gene of the hyperthermophilic bacterium
RT Thermotoga maritima cloned by complementation in Escherichia coli.";
RL Eur. J. Biochem. 216:709-715(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-MSB8 / DSM 3109;
RX MEDLINE: 99287316.
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
RN [3]
RP SEQUENCE OF 1-31.
RX STRAIN-MSB8 / DSM 3109;
RX MEDLINE: 90201029.
RA Wda A., Jaenicke R., Huber R., Stetter K.O.;
RT "Lactate dehydrogenase from the extreme thermophile Thermotoga
RT maritima.";
RL Eur. J. Biochem. 188:195-201(1990).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE: 98322364.
RA Auerbach G., Ostendorp R., Prade L., Kordorfer I., Dams T., Huber R.,
RA Jaenicke R.;
RT "Lactate dehydrogenase from the hyperthermophilic bacterium
RT Thermotoga maritima: the crystal structure at 2.1-A resolution
RT reveals strategies for intrinsic protein stabilization.";
RL Structure 6:769-781(1998).
CC -1- CATALYTIC ACTIVITY: L-LACTATE + NAD(+) -> PYRUVATE + NADH.
CC -1- PATHWAY: FINAL STEP IN ANAEROBIC GLYCOLYSIS.
CC -1- SUBUNIT: HOMOTETRAMER.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X74302; CAA52355.1;
CC EMBL: AE001823; AAD36929.1;
CC PIR: S36863; S36863.
CC PDB: 1A5Z; 23-MAR-99.
CC TIGR: TMI867.
CC INTERPRO: IPR001236;
CC INTERPRO: IPR001557;
CC PFAM: PF00056; 1dh; 1.
CC PRINTS: PR00086; LLDHRCNASE.
CC PROSITE: PS00064; L_LDH; 1.
CC Oxidoreductase; NAD: Glycolysis; 3D-structure.
CC ACT_SITE 172 172 BY SIMILARITY.
CC FT ACT_SITE 172 172
CC CONFLICT 14 14 MISSING (IN REF. 3).

```


A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0672
C:Superfamily: L-lactate dehydrogenase

Query Match 33.2%; Score 560.5; DB 2; Length 313;
Best Local Similarity 35.9%; Pred. No. 1.2e-35;
Matches 113; Conservative 72; Mismatches 119; Indels 11; Gaps 3;

OY 9 RPKIAMVSGMIGTAMFLCSRELGDVVLFDVVPMPKAMDISHNSVVDGTITVYG 68
Db 4 QPLTIIICAGVYGMATVAVMLMKGYDDLIIARTPGKPGEGALDLAHAAELGVDIRISG 63
OY 69 SNSVECLGADVITTAGITIPGSKDEMSMDLLPVNIKIMREVGAIKSYCNATVY 128
Db 64 SNSIEDMGSDIVLTATIGRPG-----MTREQLLENNANTMALAKIKAVAADATV 118
OY 129 NITNPLDVVAALQSSGLPHHRICGMAGMLDSSFRRMADKLEVSPPDVQGVYIGV 188
Db 119 ITTNPVDMATVVMKKTGFPRERIVGSGIILDSAMAYIISGLKGVSKSVAYILGHHG 178
OY 189 DHMPLSRATVNGIPLSEFVKKGWKOEEVDIVQKTKVAGETVRLLOGSAYVARGA 248
Db 179 QKMEVPLRSSVGVPLHLMK-----ETIEEVVSETVNAKITELRGY-SSNVGPA 232
OY 249 SAIGMAESYLDRKRKRVMSVSCYLOGGVGNHYGVCVIGRGVEKITELETOEHOE 308
Db 233 GLVLTVEIKRDSKRIYYSILYLOGEYGNDAVPAVIGSGIERLIELPLEDEKRK 292
OY 309 LOGSIDEVKEKOKAI 323
Db 293 FDEAVQAVKILVETL 307

RESULT 8

E69649

L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: E69649; A25805

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033

A:Accession: E69649

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-321 <KUN>

A:Cross-references: GB:299105; GB:AL009126; NID:92632457; PIDN:CAH12099.1; PID:92632591

A:Experimental source: strain 168

R:Heidiger, M.A.; Frank, G.; Zuber, H.

Biol. Chem. Hoppe-Seyler 367, 891-903, 1986

A:Title: Structure and function of L-lactate dehydrogenases from thermophilic and mesophi

A:Reference number: A25805; MUID:97076052

A:Accession: A25805

A:Molecule type: protein

A:Residues: 2-38, 'L', '40-51', 'N', '53-57', 'AP', '60-120', 'I', '122-224', 'T', '226-315', 'VN' <HED>

C:Genetics:

A:Gene: lctE

C:Function:

A:Description: catalyzes the reversible oxidation of (S)-lactate to pyruvate by NAD+
C:Superfamily: L-lactate dehydrogenase
C:Keywords: NAD: oxidoreductase
F:2-321/Product: L-lactate dehydrogenase #status experimental <MAT>
F:8-38/Region: beta-alpha-beta NAD nucleotide-binding fold
F:152,179/Active site: Asp, His #status predicted

Query Match 27.3%; Score 460; DB 2; Length 321;
Best Local Similarity 33.4%; Pred. No. 6.2e-28;
Matches 106; Conservative 69; Mismatches 124; Indels 18; Gaps 7;

OY 11 KIAMVSGMIGTAMFLCSRELGDVVLFDVVPMPKAMDISHNSVVDGTITVYG 65
Db 8 KVALGAGVGVSSVAFALINQGITDELVIDVNRKAMQDVDPHGRNF--GLQPKYT 64
OY 66 VYGSNSYELCKGADVITTAGITIPGSKDEMSMDLLPVNIKIMREVGAIKSYCN 125
Db 65 SVG--TYEDCKADADLCACANQKPG-----TLELVKRLKIFKGVSVMSGFDG 117
OY 126 FVINTNPLDVVAALQSSGLPHHRICGMAGMLDSSFRRMADKLEVSPPDVQGVYIG 185
Db 118 IFVATNPVDILTATVTKRFGSLPKRERVIGSGTLLDSARFRLSEYFGAAPQVNAHII 177
OY 186 VHGDMVPLSRATVNGIPLSEFVKKGWKOEEVDIVQKTKVAGETVRLLOGSAYV 244
Db 178 EHGDELPLVMSHANGVGVSELVKNDAYKOEELDQIVDDVKNAAVHIIE--KKGATY 235
OY 245 APGASAIOMAESYLDKRRKRVMSVSCYLOGGVGNHYGVCVIGRGVEKITELETO 304
Db 236 GVAMSLARITKAILHNENSILVSTYLDQYIGADVYIGVAVVARGIAGITTELNLNEK 295
OY 305 EROELQSIDEVKEKOK 321
Db 296 EKEQFLHSAGVILKNILK 312

RESULT 9

DEBSUM

L-lactate dehydrogenase (EC 1.1.1.27) - Bacillus megaterium

C:Species: Bacillus megaterium

C>Date: 03-Aug-1994 #sequence_revision 30-Sep-1991 #text_change 11-Jun-1999

C:Accession: S00133; S01472; A00354

R:Madwogel, S.; Weber, H.; Zuber, H.

Biol. Chem. Hoppe-Seyler 360, 1391-1399, 1987

A:Title: Structure and function of L-lactate dehydrogenases from thermophilic and mes

megaterium. Preparation and properties of a hybrid lactate dehydrogenase comprising

A:Reference number: S00133; MUID:88107005

A:Accession: S00133

A:Molecule type: DNA

A:Residues: 1-318 <NAL>

A:Cross-references: EMBL:M22305; NID:9143135; PIDN:AAA22566.1; PID:9143136

R:Stangl, D.; Wiederekhr, F.; Suter, F.; Zuber, H.

Biol. Chem. Hoppe-Seyler 360, 1157-1166, 1987

A:Title: Structure and function of L-lactate dehydrogenases from thermophilic and mes

terium.

A:Reference number: S01472; MUID:88050100

A:Accession: S01472

A:Molecule type: protein

A:Residues: 1-318 <STY>

A:Comment: This enzyme is activated by fructose-1,6-diphosphate.

C:Function:

A:Description: catalyzes the reversible oxidation of (S)-lactate to pyruvate by NAD+

C:Superfamily: L-lactate dehydrogenase

C:Keywords: homotetramer; NAD: oxidoreductase

F:1-318/Product: L-lactate dehydrogenase #status experimental <MAT>

F:11-41/Region: beta-alpha-beta NAD nucleotide-binding fold

F:154,181/Active site: Asp, His #status predicted

Query Match 27.0%; Score 455; DB 1; Length 318;
Best Local Similarity 31.7%; Pred. No. 1.5e-27;
Matches 101; Conservative 79; Mismatches 123; Indels 16; Gaps 8;

L-lactate dehydrogenase (EC 1.1.1.27) - Thermotoga maritima (strain MSB)

C:Species: Thermotoga maritima

C:Date: 22-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 18-Jun-1999

C:Accession: S36863; S36864; D72202

R:Ostermeyer, R.; Liebl, W.; Schurig, H.; Jaenicke, R.

Eur. J. Biochem. 216, 709-715, 1993

A:Title: The L-lactate dehydrogenase gene of the hyperthermophilic bacterium Thermotoga

A:Reference number: S36863; MUID:94009031

A:Accession: S36863

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-319 <OST>

A:Cross-references: EMBL:X74302; NID:9396280; PIDN:CAA52355.1; PID:9396281

A:Accession: S36864

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-31,38-53,55-85,163-173 <OS2>

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316

A:Accession: D72202

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-319 <ARP>

A:Cross-references: GB:AE001823; GB:AE000512; NID:94982441; PID:94982452; TIGR:TM1867

A:Experimental source: strain MSB

A:Genetics:

A:Gene: TM1867

A:Superfamily: L-lactate dehydrogenase

C:Keywords: oxidoreductase

Query Match 26.0%; Score 439.5; DB 2; Length 319;

Best Local Similarity 33.2%; Pred. No. 2,3e-26;

Matches 106; Conservative 64; Mismatches 134; Indels 15; Gaps 7;

11 KIAMGSGMIGTMAFLCSLRELG-DVVLFDVVPMPMKAMDISHNSVDGTGTVGS 69

2 KIGIVGLGRVGSSTFALMKGFAREMVLIDPKRAEGDLDLHGTFETRA-NIT-A 59

70 NSYECLEKADVITTAGITKIPKSDKEMSRDLPVNIKIREVGAIAKSCPNAYIN 129

60 GDVADLKSDVIVIAAGVQKPGG---TRLOLLGRNARVKEIARNVSKYAPDSIVIV 114

130 ITNPDLVVAALQESSGLPHRIGCMAGMLDSRFRMIADKLEVSPPDVQGMVIGVGD 189

115 VTNPVDVLTFFELKESGMDPRKVGSGVLDPAKRLTLAHCSESPSVHYVIGEHED 174

190 HMPLSRAATVNGIPLS---EFVKKGIKEEVDIVOKTVAGGEIVRLLOGSAYYAP 246

175 SEVPWSGAMIGIPIQNMCOICK--CDSKILENFAEKTRAAVEIIE--RKGATHAI 230

247 GASAIQMAESVIAKDKRRVWCSYLOGGYQVNHLYGPCVIGGVEKIELELTAEOR 306

231 ALAVADIVESTFPEKRVLTLSVLELYGVKLCISVPLVGLKHGVERILELNLNEEL 290

307 QELGSDIEVEMOKAIA 325

291 EAFKRSASILKNAINEITA 309

RESULT 13

H64230

L-lactate dehydrogenase (EC 1.1.1.27) - Mycoplasma genitalium

C:Species: Mycoplasma genitalium

C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999

C:Accession: H64230

R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.

M.; Fuhmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

C.A.; Venter, J.C.

Science 270, 397-403, 1995

A:Title: The minimal gene complement of Mycoplasma genitalium.

A:Reference number: A64200; MUID:96026346

A:Accession: H64250

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-312 <TIG>

A:Cross-references: GB:U39733; GB:LA3967; NID:91046177; PIDN:AAB01650.1; PID:91046180

A:Experimental source: strain G-37

C:Genetics:

A:Genetic code: SGC3

A:Superfamily: L-lactate dehydrogenase

C:Keywords: oxidoreductase

Query Match 25.7%; Score 434.5; DB 2; Length 312;

Best Local Similarity 34.2%; Pred. No. 5,4e-26;

Matches 107; Conservative 63; Mismatches 128; Indels 15; Gaps 8;

10 PKIAMGSGMIGTMAFLCSLRELG-DVVLFDVVPMPMKAMDISHNSVDGTGTVY 67

4 PKIAVSGCAVGTSPFLYAMTRALGSEMYIDINEKAKGVNFDLQDASSCPNCKVYA 63

68 GSNSECEKAGDVITTAGITKIPKSDKEMSRDLPVNIKIREVGAIAKSCPNAY 127

64 G-EYSQKDYDFEFISAG---RPQKQGE-TRLOLLGVEIEMKSIKEIKSGFNGVT 117

128 ITNPDLVVAALQESSGLPHRIGCMAGMLDSRFRMIADKLEVSPPDVQGMVIGV 187

118 LANSNPVDIMSTYTLKVTGEPKPKVIGSGTLDSALRFAIAKRYQMSKSDVQAYYIG 177

188 GDMVPLSRATVNGIPLSEFVKKGIKEE-EVDIVOKTVAGGEIVRLLOGSAYYA 245

178 GDSVSIISSAKIAGLSLKHFSKASDIKEFEGLDPIRRAY--EIIIE--RKGATFG 232

246 PGASAIQMAESVIAKDKRRVWCSYLOGGYQVNHLYGPCVIGGVEKIELELTAE 305

233 IEASADVAEQLIKDKTEVRVVAFLTLGQYAKDMFGTFCVLSRGKIEKIELEISNTE 292

306 ROELGSDIEVKE 318

293 KVALENSIKVLDK 305

RESULT 14

DELBLA

L-lactate dehydrogenase (EC 1.1.1.27) - Lactobacillus casei

C:Species: Lactobacillus casei

C:Date: 18-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 07-Feb-1997

C:Accession: A43944; J00280; A00352

R:Kim, S.F.; Baek, S.J.; Pack, M.Y.

Appl. Environ. Microbiol. 57, 2413-2417, 1991

A:Title: Cloning and nucleotide sequence of the Lactobacillus casei lactate dehydroge

A:Reference number: A43944; MUID:92117575

A:Accession: A43944

A:Molecule type: DNA

A:Residues: 1-326 <KIM>

A:Experimental source: strain ATCC 393

A>Note: sequence extracted from NCBI backbone (NCBI:77578, NCBI:77579)

R:Taguchi, H.; Ohta, T.

submitted to JIPID, November 1991

A:Reference number: J00280

A:Accession: J00280

A:Molecule type: DNA

A:Residues: 2-326 <TAG>

A:Experimental source: strain ATCC393

R:Hensel, R.; Mayr, U.; Yang, C.

Eur. J. Biochem. 134, 503-511, 1983

A:Title: The complete primary structure of the allosteric L-lactate dehydrogenase fro

A:Reference number: A00352; MUID:83287369

A:Accession: A00352

A:Molecule type: protein

A:Residues: 2-25, 'F', 27-51, 'T', 53-87, 'KQ', 90-118, 'L', 120-269, 'I', 271-272, 'L', 274-326

C:Genetics:
A:Gene: l-lct
C:Function:
A:Description: catalyzes the reversible oxidation of (s)-lactate to pyruvate by NAD+
C:Superfamily: L-lactate dehydrogenase
C:Keywords: homotetramer; NAD; oxidoreductase
F:2-326/Product: L-lactate dehydrogenase #status experimental <MAT>
F:11-41/Region: beta-alpha-beta NAD nucleotide-binding fold
F:154,101/Active site: Asp, His #status predicted

Query Match 25.6%; Score 431.5; DB 1; length 326;
Best Local Similarity 29.9%; Pred. No. 9.7e-26;
Matches 96; Conservative 82; Mismatches 132; Indels 11; Gaps 6;

QY 1 MAVFEKNTPRKIAMVSGMIGTMAFLCSLRELG-DVYLFDDVPPNMPKAMDISHNSSY 59
DB 1 MASTIDKHOKVILVGDGAVGSYAVANVLOGIAOEIGIVDFPKOTKGDADLS-NALP 59
QY 60 VDTGITVYSGNSYECLKAGADVITITAGITIKPKSDKEMSRDLPVNIKIRVGAIR 119
DB 60 FTSPKRIY-SAEYSDAKDADLVITAGAPQKRG-----TRLDLVNKNKLIKSTVDPY 113
QY 120 SYCPRAFYINTNPDLVVAALQESSGLPHNRICGMACHLSSRRRMIAADKLEVSPPDY 179
DB 114 DSGFNGITLVANPVDILTATATWKLSGFPKNRVGSGTSLDARFRQSTAEEMVNDARSV 173
QY 180 QGMVGVGDHVPPLSRATVNGIPLSEFVK-KGMIOEVDIVQTKPVAGGEIVRLIG 238
DB 174 HAYIMGEHDTPEFPWSMANIGCVTIAEYVKAHPKEDLVKMFEDVDAAYETIKL-- 231
QY 239 QGSAYYAPGASAIQMAESYLKDRKRVWCSCYLOGGYQVNHLYGVCVYIGRGVEKITE 298
DB 232 KGATFYGIATLARIKALINDENAVPLSVYMDQYGLNDIYICTPAVINNGIONILE 291
QY 299 LETAQEQLQSGIDEVYKEM 319
DB 292 TPLTDHEESMOKSASQLKV 312

RESULT 15

S08183
L-lactate dehydrogenase (EC 1.1.1.27) X - Bacillus psychrosaccharolyticus
C:Species: Bacillus psychrosaccharolyticus
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 14-May-1993
C:Accession: S08183; A38031
R:Vckovski, V.; Schlatter, D.; Zuber, H.
Biol. Chem. Hoppe-Seyler 371, 103-110, 1990
A:Title: Structure and function of L-lactate dehydrogenases from thermophilic, mesophilic
and psychrophilic bacterium Bacillus psychrosaccharolyticus.
A:Reference number: S08182; MUID:90241471
A:Accession: S08183
A:Status: not compared with conceptual translation.
A:Molecule type: DNA
A:Residues: 1-319 <VCK>
A:Accession: A38031
A:Molecule type: protein
A:Residues: 1-24 <SCH1>
C:Superfamily: L-lactate dehydrogenase
C:Keywords: homotetramer; NAD; oxidoreductase
F:1-319/Product: L-lactate dehydrogenase X #status experimental <MAT>

Query Match 25.5%; Score 431; DB 2; length 319;
Best Local Similarity 31.4%; Pred. No. 1e-25;
Matches 99; Conservative 76; Mismatches 122; Indels 18; Gaps 9;

QY 11 KIAMGSMIGCTMAFLC---SLRELGDVLEDDVPPNMPKAMDISHNSSVDTGCTV 66
DB 8 RVALIGAGSVSSYAFALNOSTE--ELVITDVNEDKAMGDANDLNKGFAPNPTKTW 65
QY 67 YGSNSYECLKAGADVITITAGITIKPKSDKEMSRDLPVNIKIRV-VGAIRKSYCPNA 125
DB 67 YGSNSYECLKAGADVITITAGITIKPKSDKEMSRDLPVNIKIRV-VGAIRKSYCPNA 125

DB 66 YG--NYDDCKEADIVICAGANOKPGE-----TRLDVLEKNLKFSLVDQVVASGFDGI 118
QY 126 FVYININPLDVVAALQESSGLPHNRICGMACHLSSRRRMIAADKLEVSPPRYQGMVIG 185
DB 119 FLI-ATNPVDILTATATWKLSGFPKNRVGSGTSLDARFRQSTAEEMVNDARSV 177
QY 186 VHDHVPPLSRATVNGIPLSEFVKKG-WIKOEVDIVQTKPVAGGEIVRLIGOGSAY 244
DB 178 EHDDELTPWSMADIGVPEELITNPEYKMDLQLEVNDAAYHIK--KSGATY 235
QY 245 APGASAIQMAESYLKDRKRVWCSCYLOGGYQVNHLYGVCVYIGRGVEKITELELTAQ 304
DB 236 GIAMGLARITKALINNENSVLTVDGEGYKOVYIGVPAVNRTGIRELIELTSET 295
QY 305 ERELQSGIDEVYKEM 319
DB 296 EOKQFTHSSTVLKEI 310

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